

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:36:49 ; Search time 32.24 Seconds

(without alignments)
700.403 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLAPAMSPPTTYLLILL...RPGQVPPVSPQDLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database : PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1242	100.0	235	I38440	flt3 ligand - huma
2	864.5	69.6	245	S43293	FLT3/FLK2 ligand (
3	834	67.1	178	I39076	FLT3 ligand altern
4	768.5	61.9	231	A49265	FLT3/FLK-2 ligand
5	606.5	48.8	220	S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	I58343	FLT3 ligand isofor
7	93	7.5	1217	T22672	hypothetical prote
8	92	7.4	661	TNBE12	74K alpha trans-in
9	89.5	7.2	387	I48201	hypothetical prote
10	89	7.2	793	S60735	adhalin - golden h
11	89	7.2	793	AB1990	splicing factor SF
12	88.5	7.1	238	T00257	hypothetical prote
13	88.5	7.1	1386	T00032	hypothetical prote
14	88	7.0	753	A32290	OP protein - Kenne
15	87.5	7.0	479	A32290	protein-tyrosine-p
16	87	7.0	910	A53137	tyrosine kinase re
17	86.5	6.9	590	A40437	glutamic acid-rich
18	86	6.9	299	T17832	hypothetical prote
19	86	6.9	485	A33647	sulfated surface g
20	86	6.9	746	T28004	hypothetical prote
21	85	6.8	289	A87646	hypothetical prote
22	85	6.8	366	A37374	Fc gamma (19g) rec
23	84	6.8	263	T03162	tegment protein 6
24	84	6.8	757	A39283	gamma-glutamyl car
25	83.5	6.7	199	E75630	hypothetical prote
26	83.5	6.7	530	A43690	transactivator EBN
27	83	6.7	1509	T19486	hypothetical prote
28	82.5	6.6	418	T19800	hypothetical prote
29	82.5	6.6	426	I36948	Ig epsilon-chain -

30	82.5	6.6	512	2	D40829	activin receptor i
31	82.5	6.6	513	2	J01484	proline/leucine-rl
32	82	6.6	106	2	T06479	hypothetical prote
33	82	6.6	854	2	T23837	hypothetical prote
34	81.5	6.6	485	2	C75460	hypothetical prote
35	81.5	6.6	488	2	S13423	stromelysin 3 (EC
36	81.5	6.6	958	2	T13593	hypothetical prote
37	81.5	6.6	1119	2	T50995	related to cytoske
38	81	6.5	196	2	B48332	cysteine-rich exte
39	81	6.5	209	2	A48232	hypothetical prote
40	81	6.5	294	2	A12016	probable transpos
41	81	6.5	388	2	S15591	ig epsilon chain C
42	81	6.5	428	1	EHHT	class I cytokinase
43	80.5	6.5	636	2	TJ0047	hypothetical prote
44	80.5	6.5	1176	2	T49482	hypothetical prote
45	80.5	6.5	1306	2	T13592	translation initia
46	80.5	6.5	1402	2	I46707	isopenicillin N ep
47	80	6.4	398	2	T52311	(S)-2-hydroxy-acid
48	80	6.4	434	2	S74706	serine/threonine k
49	80	6.4	704	2	AE2107	protein kinase C (
50	80	6.4	1174	2	T43051	

ALIGNMENTS

RESULT 1
I38440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence.revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A:title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842
A:Accession: I38440
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AA19825.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McCleanahan, T.; Zurawski, S.; Bazan, J.F.;
Felt, A.; Muench, M.; Kelnier, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', '73-235 <HAN>
A:Cross-references: GB:U0406; NID:9483844; PIDN:AA17999.1; PID:9483845
A>Note: the authors translated the codon AGT for residue 25 as Met
C:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 5.3e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAMSPPTTYLLILLSSGISTGQCSFQHSPISSDPFAVKIRLSYLLQDYPTV 60
Db 1 MTVLAPAMSPPTTYLLILLSSGISTGQCSFQHSPISSDPFAVKIRLSYLLQDYPTV 60

QY 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 Db 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPWPWSRPLEATAPT 180
 Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPWPWSRPLEATAPT 180
 QY 181 AQPPLLILLLLPVGLLLLAAMCLHMQRRTTPREGEQVPVPSPDILLVH 235
 Db 181 AQPPLLILLLLPVGLLLLAAMCLHMQRRTTPREGEQVPVPSPDILLVH 235

RESULT 2

S43293

Flt3/Flk2 ligand (clone S109) - human

C:Species: Homo sapiens (man)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C:Accession: S43293

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K&felt, A.; Muench, M.; Kelnner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994

A:Title: Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of haematopoietic A:Reference number: S43290; MUID:94195428

A:Accession: S43293

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-245 <HAN>

A>Note: the authors translated the codon AGT for residue 25 as Met

Query Match

69.6%; Score 864.5; DB 2; Length 245;

Best Local Similarity 73.0%; Pred. No. 1,1e-66;

Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 60
 Db 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 60
 QY 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 Db 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPWPWSRPLEATAPT 180
 Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPWPWSRPLEATAPT 177
 QY 181 AQPPLLILLLLPVGLLLLAAMCLHMQRRTTPREGEQVPVPSPDILLVH 237
 Db 178 WPRHGEDTEAHRGESP-----ARGCIAMTQRLKANGSLPMAPLIPSP 222
 QY 228 Q 228
 Db 223 E 223

RESULT 3

I39076

Flt3 ligand alternatively spliced isoform - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I39076

R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032381

A:Accession: I39076

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RES>

A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038

C:genetics: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.3e-64;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 60
 Db 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 60
 QY 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 Db 61 ASNQDELCGGLRWLVLAQRMERLKTAVGSKMGLLERVNTETIHVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCP 160
 Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCP 160

RESULT 4

A49265

flt3/flk-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: A49265; I49347; I49346; S43290

R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Glinski, B.; Holl Cell 75, 1157-1167, 1993

D.; Williams, D.E.; Beckmann, M.P.

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084791

A:Accession: A49265

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LYM>

A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA9436.1; PID:g439442

R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581

A:Accession: I49347

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163, 'G', '165', 'HYAG' <RES>

A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041

A:Accession: I49346

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197, 'L', '198-231 <RE2>

A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040

R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; felt, A.; Muench, M.; Kelnner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994

A:Title: Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of haematopoi

A:Reference number: S43290; MUID:94195428

A:Accession: S43290

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197, 'L', '198-231 <HAN>

A:Experimental source: clone T110

A>Note: the sequence from fig. 2c is inconsistent with that from fig. 2a in having 4-

C:Genetics:

A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;
 Best Local Similarity 70.3%; Pred. No. 1.8e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 59
 Db 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSYLLQDYPVT 60

OY VASNNODELGGGRLVLAORMMERLTVAAGSKQGLTERNEIHHVTCAFOPPSC 119
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db VAANNQDERHCKALMSLEFLAQRMIEQLKTVAAGSKQGLTEBYNTEIHVYTCTPPLPEC 120

OY LRFVOTNISRLLOESBQVALAKPWITR--QNFSCLBELCQPDSSTLPKPSRPPLFAT 177
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db LRFVOTNISHLKDPTQTALAKPCIGRAQONFSCLTEOCOPDSTLLPPSPPLATEAT 180

OY AFTAPQPP-LILLILFPVGILLLAAANCLHMORTRRRTPRPGECVPVPSD 227
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db ELFRPAPQGLLLLLLLLPIYLVLAAANGLNQRARR---GELHPGVPLP 228

```

RESULT      5
S43291
FLR3/FLK2 ligand (clone T118) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43291
R:Hannum, C.; Sulpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Wuensch, M.; Keisner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
A:Title: Ligand for FLR3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43291
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <HANO>

```

	Query Match	48.8%	Score 606.5	DB 2	Length 220
	Best Local Similarity	61.5%	Pred. No. 1,2e-44		
	Matches 134	Conservative 18	Mismatches 43	Indels 23	Gaps 5
QY	1	MTVLPASP--TYYIIIIIIIISSGLSGDQCSFQSPSPSPFAVYIRLSYLDQDYVT	59		
Db	1	MTVLPASPNSPNSLLHLLHLLSPCLRGTPDCYFHSNPSSNKVAFRELIHDLIDYVT	60		
QY	60	VASNTQDELLCGGLRVLVAQRMERLKTIVAGSKKQGLIERVNIYTHVTKCAFOPPSC	119		
Db	61	VAVNLDQDEHCAALMSLFLAQRMVQLKTIVAGSKKQGLIEDVNIYTHVTKCAFOPPSC	120		
QY	120	LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSSTLPWPSPRP----	173		
Db	121	LRFVQTNISHLKDKCTQLLALPCIGKACQNFSCLELVQCCPDSSSTLPWPSPRP----	174		
QY	174	--LEATAPAPQPPILL-----LILLPVGLLLAA	201		
Db	175	ATRLTATALLVCPGLLPLVGTSHMFLPYFLSLSS	212		

```

RESULT 6
158343
flt3 ligand isoform 5H - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: 158343
R:Lyman, S.D.; James, L.; Escobar, S.; Doney, H.; de Vries, P.; Brassel, K.;
Oncogene 10, 149-157, 1995
A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand
A:Reference number: 158343; MUID:95124710
A:Accession: 158343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-220 <RES>
A:Cross-references: GB:S76459; NID:g913479; PIDN:AAH33069.1; PID:g913480

```

Query Match 48.8%; Score 606.5; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 1.2e-44;
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

```

Db      1  MTVLAPAMSPNSLLILLILLSPCLRGTPDCFTSPSSNKVAFRELIIDLLDYEPT  60
QY      60  VASNIQDEELCGGLRLVLAQRMERLEITVAGSKQGLIERVNTIEIHFVYCAFOPPSC  119
Db      61  VAVNIQDEEHCKALMSLFLAQRWIEQLKTIVAGSKQOTLEDVNTIEIHFVTSCTFOPLPEC  120
QY      120  LRFVQTNISRLQEQENSEQLVALKPWITR--QNFSCRLELQCPDSDSTPPPPSPPP----  173
Db      121  LRFVQTNISHLKDKCTQLTALAKPIGKACQNFSCRLEVQCPGNG-----GPAQIHNG  174
QY      174  ---LEATAPTAQPPULL-----LILLPVGLLLAA  201
Db      175  ATRLTATALLVCPGILLPLVGTSHMFLPFLPLSLSS  212

```

```

RESULT      7
T22672
hypothetical protein F54F12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22672
R:Barlow, K
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19597
A:Accession: T22672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1217 <MIL>
A:Cross-references: EMBL:Z81548, NID:e1062020, PIDN:CAE04464.1; GSPDB:GN00021; CESP:R.1
A:Experimental source: clone F54F12
C:Genetics:
A:Gene: CESP:F54F12.1
A:Map position: 3
A:Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

```

```

Query Match Similarity 7.5%; Score 93; DB 2; Length 1217;
Best Local Similarity 23.6%; Pred. No. 8;
Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERLKTAVGSKKQGL---LERYNTEIHETVTKCAFPPEPSCLEFYVOTNISRLLOETSEOLV 139
   | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 627 MONAVKAVDGTCKSSVIDALEKLSITMDLDQKKKKFEAPATLKAML---FFASVASNIA 682

QY 140 ALKPWITTRONFSRCLTELQCPDPSITL---PPPMSPRLPEATAPAP---OPILILLIL 191
   || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 683 ALRPQGTTSDDPAAPAVPPIPNKKGSLINGNPSSPLLIPVASSPAPATPEESNMILYII 742

QY 192 LPEVGLILLAA-----AMCLHMORTRRKRTPRGEOYPPVPSF 227
   || | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 743 GAVGGLLVAALIGVILFEVFEQKKKKKEDKPD--PPAPLP 781

```

RESULT 8
TNBEL2
77k alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: C27342
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657
A:Accession: C27342
A:Molecule type: DNA
A:Residues: 1-661 <DAV>
A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001
C:Genetics:
A:Gene: 12
C:Superfamily: herpesvirus 77k alpha trans-inducing protein
C:Keywords: trans-inducing protein; transcription regulation

R;Simister, N.E.; Mostov, K.E.

Nature 337, 184-187, 1989

A;Title: An Fc receptor structurally related to MHC class I antigens.

A;Reference number: S02117; MUID:89097257

A;Accession: S02117

A;Molecule type: mRNA

A;Residues: 1-366 <ST2>

A;Cross-references: EMBL:X14323; NID:956436; PIDN:CAA32503.1; PID:956437

A;Note: part of this sequence, including the amino end of the mature protein, was confli

C;Superfamily: class I histocompatibility antigen: immunoglobulin homology

C;Keywords: immunoglobulin receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-366/Product: IgG Fc receptor 51k chain #status predicted <MAT>

Query Match 6.8%; Score 85; DB 2; Length 366;

Best Local Similarity 22.2%; Pred. No. 9.9;

Matches 51; Conservative 21; Mismatches 66; Indels 92; Gaps 11;

```

QY 46 RELSDYLQDPYTVASNLQDELICGGLMRLVLAQRWME---RLKTVAGSKMGGLEERV 101
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 173 RKESEFLITSCP-----ERLLGHLERGRQNLWEKPEPSMRLLKARPGNSGSSVL--- 220
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 102 NTEIHFTYKCA---FQPPSCIRFVQTNISRLQETSEQLVALKPWITRQNFSC----- 153
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 221 -----TCAAFSFYPELKFRLKNGLA-----SGSGMCSGCPN 253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 154 -----LEL-----QCQPDSSSTLPPWSPRPLEATAPARQPLLLLLLPVG 195
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 254 GDGSFHAMSLLEVKRGDEHHYQCQVEHGLAQPLT---VDDLSPARSSVPPVGIIL---G 307
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 196 LLLIA---AAMCLHWQTRRRTPR-----PGQVPPVPVSPQ 228
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 308 LLVVAAGVGLLNMNRSGLPAPWLSLGGDSGDLPGGNLPPEAEAPQ 357
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 23

tegument protein 67 - alcelaphine herpesvirus 1

C;Species: alcelaphine herpesvirus 1

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C;Accession: T03162

R;Essner, A.; Pfanz, R.; Fleckenstein, B.

J. Virol. 71, 6517-6525, 1997

A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.

A;Reference number: 214840; MUID:97404659

A;Accession: T03162

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-263 <ENS>

A;Cross-references: EMBL:AF005370; NID:92337967; PIDN:AAC58114.1; PID:92338030

C;Superfamily: human herpesvirus 4 BRF1 protein

Query Match 6.8%; Score 84; DB 2; Length 263;

Best Local Similarity 25.3%; Pred. No. 8.3;

Matches 55; Conservative 30; Mismatches 84; Indels 48; Gaps 10;

```

QY 8 WSPPTVILLILSSGSGTQDCSFQHSPISSDAVAKIRELSVILQDPYTVASNLQDE 67
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
Db 77 FSPF-----FTCNNGGLAVTLK-----YSEPRDISRYGQATSNALVNLQRN 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 ELGGLMRLVLAQRWMERLKT-----VAGSKM--QGILLERVNTIEHFVTCARQPP 116
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
Db 122 SF-----VVLSDQDFIKFPTPLVFARQDITNSMVCRTVLTSSRNSLQFLV--VSKN 173
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
QY 117 PSCLRFVQTNISRLQETSEQLVALKPWITRQNFSCLEL--QCQPDSSSTLPPWSPRPLE 175
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 PRRLENIWDMIKRAVEATGSLPA-----TRE---KPLPLEQTEQLSTLPSGHLRLVQ 225
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 176 ATAPTAQPP-----LLILLPLVGLILLAAWCLHW 207
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 226 STSLTGRCPSWGACALLLLSLAVGLMAIILAKIMQW 262
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 24

gamma-glutamyl carboxylase (EC 4.1.1.-) - human

A39283

C;Species: Homo sapiens (man)

C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 06-Dec-1996

C;Accession: A39283

R;Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.

Science 254, 1634-1636, 1991

A;Title: Cloning and expression of the cDNA for human gamma-glutamyl carboxylase.

A;Reference number: A39283; MUID:92086858

A;Accession: A39283

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A;Molecule type: mRNA

A;Residues: 1-757 <WTA>

A;Cross-references: GB:M81592

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 6.8%; Score 84; DB 2; Length 757;

Best Local Similarity 22.3%; Pred. No. 28;

Matches 50; Conservative 29; Mismatches 59; Indels 86; Gaps 13;

```

QY 3 VLAAMSPTTYLLILLSSGSGTQDCSFQHS-----PISDFA---VKIRELSDYL--- 52
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 488 IVQAAWSP-----FQRTSWQVPLNDLSPPRAKLOELKSSLDNN 526
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 53 -----LQDPYTVASNLQDELICGGLMRL-----VLAQRWMERLKTVAGSKM--G 96
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 527 TEVVFIADEPGLNLENVSEDLGNTSIQLQGEVTELVAAQKQKQTLR--BGEKMQLPAG 584
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 97 LLEVRNTEIHFTYKCAQPPPSCLRFVQTNISRL-----LOETSEQLVALKPWITRQ 148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 585 EYMKVYTT-----SPSPCYMYVYVNTTELAEQDLAYLQELKRY-----E 626
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 149 NFRCLQLQCPDSSSTLPPWSPRPLEATAPARQPP-PLLLLL 191
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
Db 627 NGS-----ETGPLEPPELQPL-LEGEVKGGEPPPLVQVTF 660
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 25

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: E75630

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896

A;Accession: E75630

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-199 <MID>

A;Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12655.1; PID:96460951; TIGR:DR

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRB0112

A;Map position: megaplasmid

A;Genome: plasmid

A;Note: plasmid MP1

Query Match 6.7%; Score 83.5; DB 2; Length 199;

Best Local Similarity 27.3%; Pred. No. 6.6;

Matches 47; Conservative 29; Mismatches 57; Indels 39; Gaps 13;

```

QY 75 RLVAQOR-IMMERLTVAGSKMGGLEERVNTEIHFTYKCAQPPPSCLRFVQTNISRLQ 133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 50 RLSTAQRTWQQTALTRISQVRSYSDR-----HGV---MTQPD--VTIYQSGGR---- 94
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

QY 134 TSEQVAKPWITRONFS---RCLELOCQP--DSSTLPPWSPR--PLEATAPTAQPP 185
   : | : | | : : | : | : | : | : | : | : | : | : | : | : | : |
Db 95 -NYGIALDP-LSDNNYRTSFNAYQRSIQPYQESTVPLVEFDPONPGQSALSLTRSTPP 152
QY 186 LLLLL-----LLPYGILLAAACLIHQRTRR--TPRGEQ-VPVPSPQD 229
   | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 153 LSLMLGVTEFLGLGSLIGARM-----RTKRQIVTKPGHODAKGSPGPRD 199

```

Search completed: August 6, 2002, 09:40:23
 Job time: 214 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compgen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:39 ; Search time 16.81 Seconds

(without alignments)
541.291 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MRYLAPMSPTTYLLLLLLL.....RPGQVPPVSPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1242	100.0	235 1 FL3L_HUMAN	P49771 homo sapien
2	768	61.8	232 1 FL3L_MOUSE	P49772 mus musculu
3	92	7.4	661 1 AT12-VAVD	P09264 varicella-z
4	89.5	7.2	941 1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387 1 SGCA_MESAU	O64255 mesocricetu
6	89	7.2	793 1 S3A1_HUMAN	O15459 homo sapien
7	87.5	7.0	415 1 TNF3_MOUSE	P50284 mus musculu
8	87.5	7.0	479 1 MP1P_DROME	P20483 drosophila
9	87	7.0	910 1 DDRI_RAT	O63474 rattus norv
10	87	7.0	911 1 DDRI_MOUSE	O03146 mus musculu
11	86.5	7.0	1394 1 CNG4_BOVIN	O28181 bos taurus
12	86	6.9	485 1 SSGP_VOICA	P21997 volvox cart
13	85	6.8	282 1 ATFS_HUMAN	O97401 homo sapien
14	85	6.8	366 1 FCCN_RAT	P13599 rattus norv
15	84.5	6.8	3726 1 ABR1_MOUSE	O61329 mus musculu
16	84	6.8	582 1 MNT_HUMAN	O99583 homo sapien
17	84	6.8	732 1 YF48_HUMAN	O99583 homo sapien
18	83.5	6.7	671 1 Z282_HUMAN	O99583 homo sapien
19	83	6.7	758 1 VKGC_HUMAN	P38435 homo sapien
20	81.5	6.6	488 1 MMT1_HUMAN	P24347 homo sapien
21	81.5	6.6	591 1 MNT_MOUSE	O08789 mus musculu
22	81.5	6.6	2124 1 Y197_HUMAN	O93074 homo sapien
23	81	6.5	283 1 ATFS_MOUSE	O70191 mus musculu
24	81	6.5	387 1 SGCA_MOUSE	P82350 mus musculu
25	81	6.5	428 1 EPC_HUMAN	P01854 homo sapien
26	81	6.5	1248 1 DIAL_HUMAN	O60610 homo sapien
27	80.5	6.5	1402 1 IF4G_RABIT	P41110 coryctolagus
28	80	6.4	397 1 CEF2_STRCL	P18549 streptomyces
29	80	6.4	940 1 KRC2_RAT	O08871 rattus norv
30	80	6.4	1174 1 KRC2_MOUSE	O42632 cochliobolu
31	80	6.4	1794 1 YAVI_SCHPO	O10172 schizosacch
32	79	6.4	805 1 YGW6_YEAST	P53086 saccharomyc
33	78.5	6.3	251 1 HXB4_HUMAN	P17483 homo sapien

34	78.5	6.3	382 1 AVRB_RAT	P38445 rattus norv
35	78.5	6.3	387 1 SGCA_RABIT	O28686 coryctolagus
36	78.5	6.3	913 1 DDRI_HUMAN	O08345 h epithelia
37	78.5	6.3	1180 1 ATY1_HUMAN	O9941 homo sapien
38	78	6.3	205 1 CYSR_SYNY3	O55854 synechocyst
39	78	6.3	566 1 TS13_MOUSE	O01755 mus musculu
40	77.5	6.2	1885 1 FAS2_CANAL	P43096 c fatty aci
41	77.5	6.2	2004 1 MO2_HUMAN	O27794 homo sapien
42	77	6.2	195 1 CORA_HPBVF	P29178 hepatitis b
43	77	6.2	316 1 CDNC_HUMAN	P49318 homo sapien
44	77	6.2	367 1 MREC_ECOLI	P16926 escherichia
45	77	6.2	478 1 BM3B_HUMAN	P55107 homo sapien
46	77	6.2	742 1 PKWA_THECU	P49695 thermomnos
47	77	6.2	872 1 SYV_HELPT	O92461 heliobacte
48	76.5	6.2	362 1 OPRR_CHICK	P22329 gallus gall
49	76.5	6.2	498 1 MEFA_MOUSE	O60929 mus musculu
50	76	6.1	190 1 BCT7_SHEEP	P50415 ovis aries

ALIGNMENTS

RESULT 1	FL3L_HUMAN	STANDARD:	PRT: 235 AA.
ID	FL3L_HUMAN		
AC	P49771;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3 ligand).		
CN	FL3L3C.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
XP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94195428; PubMed=8145851;		
RA	Hannum C., Cuipepper J., Campbell D., McLanahan T., Zurawski S.,		
RA	Bazan J.F., Kasteler R., Hudak S., Wagner J., Matson J., Luh J.,		
RA	Duda G., Matlika N., Peterson D., Menon S., Shanaleit A.,		
RA	Mench M., Relner G., Nankawa R., Rennick D., Roncarolo M.G.,		
RA	Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;		
RT	"Ligand for FL3L/FLK2 receptor tyrosine kinase regulates growth of		
RT	hematopoietic stem cells and is encoded by variant RNAs.";		
RL	Nature 368:643-646(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94235842; PubMed=8180375;		
RA	Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,		
RA	Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;		
RT	"Cloning of the human homologue of the murine flt3 ligand: a growth		
RT	factor for early hematopoietic progenitor cells.";		
RL	Blood 83:2795-2801(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.		
RX	MEDLINE=96032581; PubMed=7566977;		
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,		
RA	Escobar S.;		
RT	"Structural analysis of human and murine flt3 ligand genomic loci.";		
RL	Oncogene 11:1165-1172(1995).		
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC		
CC	CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING		
CC	FACTORS AND INTERLEUKINS.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM		
CC	IS ALSO PRODUCED BY ALTERNATIVE SPLICING.		
CC	-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE		
CC	SPLICING.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U04806; AAA1799.1; -
DR EMBL; U03858; AAA19825.1; -
DR EMBL; U29874; AAA90949.1; -
DR EMBL; U29874; AAA90950.1; -
DR MIM; 600007; -
DR InterPro: IPR004213; flt3_1lg.

DR Pfam; PF02947; flt3_1lg; 1.
CYTOKINE; Glycoprotein; Transmembrane; Alternative splicing; Signal.
KW SIGNAL
FT CHAIN 1 26
FT SIGNAL 1 26
FT CHAIN 27 235
FT SIGNAL 27 235
FT CHAIN 27 184
FT SIGNAL 27 184
FT CHAIN 185 205
FT SIGNAL 185 205
FT CHAIN 206 235
FT SIGNAL 206 235
FT CHAIN 126 126
FT SIGNAL 126 126
FT CHAIN 149 149
FT SIGNAL 149 149
FT CHAIN 161 178
FT SIGNAL 161 178
FT CHAIN 179 235
FT SIGNAL 179 235
FT CHAIN 72 72
FT SIGNAL 72 72
FT CHAIN 235 AA; 26416 MW; 73895BF693B4CECF CRC64;
SEQUENCE

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. Je-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAPMSPTTYLLDLLLLSSGSGTQDSFQHSPISSDPFAKIRELSDYLLQDYPTV 60
DB 1 MTVALPAPMSPTTYLLDLLLLSSGSGTQDSFQHSPISSDPFAKIRELSDYLLQDYPTV 60
QY 61 ASNQDELTCGMLRYLAQRMRRLKTVAGSKMGLLEVNNEHFVTKCAQPPPSCL 120
DB 61 ASNQDELTCGMLRYLAQRMRRLKTVAGSKMGLLEVNNEHFVTKCAQPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPWITRQNFSCLELOCOPDSSSTLPPSPRLEATPT 180
DB 121 RFVQTNISRLQETSEDLVALKPWITRQNFSCLELOCOPDSSSTLPPSPRLEATPT 180
QY 181 APOPPILLLLPYGLLLIAAWCLHMQRRTRRPRGEGVPPVPSODLLVEH 235
DB 181 APOPPILLLLPYGLLLIAAWCLHMQRRTRRPRGEGVPPVPSODLLVEH 235

RESULT 2

FL3L_MOUSE STANDARD; PRT; 232 AA.

AC PA9772;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3 DE ligand).
GN FLT3LG OR FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; Pubmed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bada J.F., Kastelein R., Hudak S., Wagner J., Matsun J., Luh J., Muench M., Kelnier G., Namikawa K., Kennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubrenil P., Birnbaum D., Lee F.;
RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SL/T;
RX MEDLINE=94084791; Pubmed=7505204;
RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKeena H.J., Splet R.R., Fletcher F.A., Maraskovsky E., Farrah T., Foxworth D., Williams D.E., Beckmann M.P.;
RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.";
RL Cell 75:1157-1167(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96032581; Pubmed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95124710; Pubmed=7824267;
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P., Brasel K., Stocking K., Beckmann M.P., Copeland N.G., Cleveland L.S.;
RT "Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs.";
RL Oncogene 10:149-157(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

RT GABABR1.";
 RL Mol. Cell. Neurosci. 13:180-191(1999).
 RP [7]
 RX R1A-R2 INTERACTION.
 RP MEDLINE-99175124; PubMed-10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Echier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity".
 RL J. Biol. Chem. 274:7607-7610(1999).
 RL [8]
 RP R1A-R2 INTERACTION.
 RX MEDLINE-20237752; PubMed-10773016;
 RA Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,
 RA Johnson M.P., Hebert T.E., Echier N., Bellay M., Metters K.,
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
 RT receptors with truncated receptors and metabotropic glutamate
 RT receptor 4 supports the GABA(B) heterodimer as the functional
 RT receptor".
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
 RL -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
 CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AJ012188; CAA09942.1; -
 DR EMBL: AF056085; AAC63228.1; -
 DR EMBL: AF095723; AAC63383.1; -
 DR EMBL: AF095724; AAC63384.1; -
 DR EMBL: AF095784; AAD30389.1; -
 DR EMBL: AF074483; AAD03336.1; -
 DR EMBL: AF069755; AAC99345.1; -
 DR EMBL: AF099033; AAD45867.1; -
 DR InterPro: IPR001828; ANF_receptor.

DR InterPro: IPR000337; GPCR_Mgr.
 DR Pfam: PF000003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 2.
 DR PRINTS: PR00248; GPCRMR.
 DR PRINTS: PR01176; GABABRECEPTR.
 DR PRINTS: PR01177; GABAB1RECEPTR.
 DR PRINTS: PR01178; GABAB2RECEPTR.
 DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 DR PROSITE: PS00982; G_PROTEIN_RECEP_F3_4; 1.
 DR G-protein coupled receptor; Transmembrane; glycoprotein; Signal;
 KW Postsynaptic membrane; Coiled coil; Alternative splicing;
 KW Polymorphism.
 FT SIGNAL 1 41
 FT CHAIN 42 941
 FT
 FT DOMAIN 42 483
 FT TRANSSEM 484 504
 FT DOMAIN 505 522
 FT TRANSSEM 523 543
 FT DOMAIN 544 551
 FT TRANSSEM 552 572
 FT TRANSSEM 573 597
 FT DOMAIN 598 618
 FT TRANSSEM 619 654
 FT TRANSSEM 655 675
 FT DOMAIN 676 691
 FT TRANSSEM 692 712
 FT DOMAIN 713 720
 FT TRANSSEM 721 741
 FT DOMAIN 742 941
 FT CARBOHYD 90 90
 FT CARBOHYD 298 389
 FT CARBOHYD 389 404
 FT CARBOHYD 404 453
 FT CARBOHYD 453 453
 FT VARSPLIC 902 927
 FT VARSPLIC 929 941
 FT
 FT VARIANT 628 628
 FT
 FT VARIANT 869 869
 FT
 FT CONFLICT 6 6
 FT CONFLICT 12 12
 FT CONFLICT 424 424
 FT SEQUENCE 941 AA; 105821 MW; 09F173DB0673C5D CRC64;
 SQ
 Query Match 7.2% Score 89.5; DB 1; Length 941;
 Best Local Similarity 44.1% Pred. No. 5.6;
 Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;
 QY 170 SRRPLEATAPTAPOPP-----LILLILLPVGLLLAAACWLMQRTTRTPPGGQVPPV 224
 DB 3 SRRSGGQPPPPPPPPPPPPARLLILLILLPLAAGM--GW---AKGAPPPSSPPL 56
 RESULT 5
 SCGA_MESAU STANDARD; PRT: 387 AA.
 ID SCGA_MESAU
 AC 064255;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-sarcoglycan precursor (Alpha-SG) (Adh1in) (50 kDa dystrophin-
 DE associated glycoprotein) (50DAO).
 GN SCGA.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

```

OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRIAN; TISSUE=Heart muscle;
RA MEDLINE=98054328; PubMed=9391120;
RA Sakamoto A., Ono K., Abe M., Jamin G., Eki T., Murkami Y.,
RA Masaki T., Toyooka T., Hanaoka F.;
RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation
RT of the same gene, delta-sarcoglycan, in hamster: an animal model of
RT disrupted dystrophin-associated glycoprotein complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FLB; TISSUE=Skeletal muscle;
RA MEDLINE=95278335; PubMed=7758576;
RA Roberts S.L., Campbell K.P.;
RT "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic
RT hamster.";
RL FEBS Lett. 364:245-249(1995).
CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF
CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMAL
CC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND
CC HEART MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D83651; BAAL2025.1; -
DR EMBL; U21677; AAA81645.1; -
KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 387
FT DOMAIN 24 290 ALPHA-SARCOGLYCAN.
FT TRANSSEM 291 311 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 312 387 POTENTIAL.
FT DOMAIN 209 335 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 174 174 CYS-RICH.
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.28; Score 89; DB 1; Length 387;
Best Local Similarity 23.48; Pred. No. 2.3;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYLLLLSSGLSTGDSFQHSPISSDFAVKIRELSYLDYLDYVYVYASNLQDEELC 70
DB 115 TTRGRLLLLI-----EDDEGRRLPYQAEFLVRSNDVEVL-----PSTPANRFL--TAL 161
QY 71 GGIWRL-----VLAQRMRERLKTAVAGSKMGLLERVNTETHEVT-----K 110
DB 162 GGIMELGELDLNLTSTALDRGCRVPLPIEGRKEGYIKVGSAPRFSTCLKMAVSPDSYAR 221
QY 111 CARQPP--SC-----LRFVGTNISRLQLQHSSEDLVALKPMTITQNSRCLQEQPD 161
DB 222 CAQGQPLLSCYSLAPHFVDMCNVSLVDKSVPEPD-----EVPDPD 266
QY 162 SSTLPWPWSRPLEAT-----APTAPQPPLLLLLLPVGLLLLLAANC----- 204
DB 267 GILEHDPFPCPPPEATGRDLADLVTLVPLLVALL---TLLAVYIMCRRREGOLKRD 323
QY 205 -----LHMQRTRRRKTPR-----GQVPP-VPSPQ-DLL 231

```

```

DB 324 MATSDIQMVHCHTIGHNTEBLROMAARREVPPLSTLPWFNVRTGERLPPEVDSAQVPLI 383
QY 232 LVEN 235
DB 384 LDQH 387

RESULT 6
S3AL_HUMAN STANDARD; PRT; 793 AA.
ID S3AL_HUMAN
AC 015459;
DT 01-NOV-1997 (rel. 35, Last sequence update)
DE 01-MAR-2002 (rel. 41, Last annotation update)
DE Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP
DE 114) (SF3A120).
GN SF3A1 OR SAP114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96079958; PubMed=7489498;
RA Kraemer A., Kulhauser F., Weisig C., Groning K., Bilbe G.;
RT "Mammalian splicing factor SF3A120 represents a new member of the
RT SURP family of proteins and is homologous to the essential splicing
RT factor PRP212 of Saccharomyces cerevisiae.";
RL RNA 1:260-272(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Alnough R., Almeida J.P., Babbage A.,
RA Baguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Blakey S., Bridgman A.M., Buck D., Burgess J., Burrill W.D.,
RA Burton V., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
RA Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,
RA Grahnam D., Griffiths M.N., Hall C., Hall R., Hall-Tremay G.,
RA Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Keshaw J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Leverha M.A.,
RA Lloyd C., Lloyd D.M., Martyn I.D., Mashheghl-Mohammadi M.,
RA Matthews L., Mccann O.T., Mccay J., Mclaren S., Mcmurray A.A.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Phillips B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Stewart C.A.,
RA Suston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M.,
RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Wilner T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Beck S., Rogers J., Shimizu N., Minooshima S., Kawasaki K., Saeki T.,
RA Asakawa S., Kudoh J., Shitani A., Shibuya K., Yoshitaki Y., Aoki N.,
RA Mitsuyma S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Lal H., Lao H.I., Lewis J., Lewis S., Jin S.-P., Loh P., Malaj S.,
RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingford D.,
RA Wu H., Yao Z., Zhan M., Zhang G., Chisoe S., Murray J., Miller N.,
RA Mix P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P.,
RA Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K.,
RA Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurehashi H., Salta S.,
RA Budarf M.L., Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanaki J.P.,
RA Peyrard M., Kedia D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilihan Y., Wright H.;
RT "The DNA sequence of human chromosome 22."

```

```

RL Nature 402:489-495(1999).
RN [3]
RX CHARACTERIZATION OF THE SPLICEOSOME.
RX MEDLINE=20337962; PubMed=10882114;
RA Das R., Zhou Z., Reed R.;
RT "Functional association of U2 snRNP with the ATP-independent
RT spliceosomal complex E.";
RT Mol. Cell 5:779-787(2000).
CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
CC THREE SUBUNITS: SF3A1/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
CC INTERACTS WITH SF3A3.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X85237; CAA59494.1; -
DR EMBL; AC004997; AAC23435.1; -
DR MIM; 605595; -
DR InterPro: IPR000061; Surp.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam; PF01805; Surp; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
KW Spliceosome; mRNA processing; mRNA splicing; Nuclear protein; Repeat.
FT REPEAT 52 94
FT REPEAT 166 208 SURP MOTIF 2.
FT DOMAIN 707 793 UBQUITIN-LIKE.
FT DOMAIN 10 16 POLY-PRO.
FT DOMAIN 118 122 POLY-GLN.
FT DOMAIN 260 267 POLY-GLU.
FT DOMAIN 369 372 POLY-PRO.
FT DOMAIN 557 560 POLY-PRO.
FT DOMAIN 672 675 POLY-PRO.
SQ SEQUENCE 793 AA; 88886 MW; 725991EC4577305C CRC64;

```

```

Query Match 7.28; Score 89; DB 1; Length 793;
Best Local Similarity 22.38; Pred. No. 5.1;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

```

```

OY 4 LAPAMSPYTLILLLLSSGLSTQDSFQHSPISSDFAVKIRELDYLLQDYPVTVAASN 63
DB 401 LPPAPADELYL-----SPITGE-----KI-----PASK 424
OY 64 LQDEELCGGLRWLYLAQRME-RLKTV-----AGSKMGLLEVNTEIHF 107
DB 425 MOEHNRIG-----LLDRRWLEQRDRSIREKQSDDEVAYPGIDIESSIKQLAER-RDIFG 478
OY 108 VTKCA-----FOPPPSGLR-----VQNIISRLQETSEQLVAKPMI 145
DB 479 VETFAIKKIGEEIQRPEEKVTDHSGSMARTQAQAQANIT--LQEOLEAIHKAKGLV 536
OY 146 -----SRCTLEQOC-----DSSTLP-----PPWSRPLEAT-----APT 180
DB 537 PEDTKEKIGSKPNEIPQDPPPSATNIPSSAPLITVPRPTMPPTVIVSAVPV 596

```

```

OY 181 APOPELLILLPYGLLLAAACLIHQRR-----RTRPRGEQVP---VSPS 227
DB 597 MPRPMASVVALPPGSVIAPMPILIHAPRIWVMPSPAPIMAPRPPMIVTAFFVPAP 656

```

RESULT	7	TRN3_MOUSE	STANDARD;	PRT;	415 AA.
AC	TRN3_MOUSE				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Lymphotoxin-beta receptor precursor.				
GN	LTBR OR TNFR OR TNFRSF3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN-CVB; TISSUE=Lung;				
RX	MEDLINE=96072804; PubMed=7594541;				
RA	Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,				
RA	Browning J.L., Ware C.F.,				
RT	"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,				
RT	and expression.";				
RL	J. Immunol. 155:5280-5288(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96163885; PubMed=8586432;				
RA	Nakamura T., Tashiro K., Nakano T., Sasayama S.,				
RA	Honjo T.;				
RT	"The murine lymphotoxin-beta receptor cDNA: isolation by the signal				
RT	sequence trap and chromosomal mapping.";				
RL	Genomics 30:312-319(1995).				
CC	-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN				
CC	IMMUNE DEVELOPMENT.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U29173; AA68964.1; -				
DR	EMBL; L38423; AB00846.1; -				
DR	EMBL; U30798; AA81334.1; -				
DR	HSSP; P25942; 1CDF.				
DR	MGI; MGI:104875; Ltbr.				
DR	InterPro: IPR01368; TNFR_C6.				
DR	Pfam; PF000771; TNFR_C6; 1.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.				
DR	PROSITE; PS00500; TNFR_NGFR_2; 3.				
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal.				
FT	SIGNAL 1 30				
FT	CHAIN 31 415				
FT	DOMAIN 31 223				
FT	TRANSMEM 224 244				
FT	DOMAIN 245 415				
FT	REPEAT 42 81				
FT	REPEAT 82 124				
FT	REPEAT 125 170				
FT	REPEAT 171 213				
FT	REPEAT 214 253				
FT	DISULFID 43 58				
FT	DISULFID 59 72				
FT	DISULFID 62 80				

FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;
 Best Local Similarity 24.4%; Pred. No. 3.3;
 Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAPPPSCL-----RV-----QINISRLQTSQVALKPMITRONFS 151
 DB 123 ECRCPGMSGVILNCEVHCBEERVLVCPGTEAEVTDVNCVPCRGHONTSS 182
 QY 152 RCLLECCPDSSSTLPPEWSPRPLEATAP-----TAPQPLLLLLLPVGLL--- 198
 DB 183 P--RACQGHTRC-----EIOGLVEARQTSYSDTICKNPPPGMALLAILSLVLEFL 235
 QY 199 ----IAANCLHWQRT-----RRTPRGCVPPVPSQ 228
 DB 236 FTTVLACAMWRHPSLCRKLGLTKRHP-GEESPCCAPR 274

RESULT 8
 MRIP_DROME STANDARD; PRT; 479 AA.
 AC P20483; Q9VAL9;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE M-phase inducer phosphatase (EC 3.1.3.48) (String protein) (Cdc25-1-like protein).
 GN SFG OR CDC25 OR CG1395.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69195217; PubMed=2702688;
 RA Edgar B.A., O'Farrell P.H.;
 RT "Genetic control of cell division patterns in the Drosophila embryo."
 RL Cell 57:177-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9106056; PubMed=2120044;
 RA Jimenez J., Alphey L., Nurse P., Glover D.M.;
 RT "Complementation of fission yeast cdc2ts and cdc2ts mutants
 RT identifies two cell cycle genes from Drosophila: a cdc2 homologue and
 RT string".
 RL EMBO J. 9:3565-3571(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anandakrishnan P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champé M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale U., Bayraktaroglu L., Beaskey E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gebhart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin M., Houston K.A., Howland T.J., Mei M.-H., Ikegami C.,
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mikhaylov G., Milshina N.V., Mobarry C., Moritz J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacile J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
 CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
 CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
 CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
 CC AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC CC
 DR EMBL; M24909; AAA28916.1; -;
 DR EMBL; X57495; CAA0732.1; -;
 DR EMBL; AE003768; AAF56885.1; -;
 DR PIR; A32290; A32290.
 DR PIR; S12008; S12008.
 DR HSSP; P30305; 10B0.
 DR Flybase; FBgn0003525; stg.
 DR InterPro; IPR000751; MPI_Phosphatase.
 DR InterPro; IPR001763; Rhodanese_domain.
 DR Pfam; PF00581; Rhodanese.
 DR PRINTS; PR00716; MRIPHPRTASE.
 DR SMART; SM00450; RHOD; 1.
 DR Cell division; Mitosis; Hydrolyase.
 KW SMART; 379 379 BY SIMILARITY.
 FT ACT_SITE 379 379
 FT CONFLICT 228 228 A -> T (IN REF. 1).
 FT FT
 SQ SEQUENCE 479 AA; 54094 MW; 68483F3A285962CC CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 479;
 Best Local Similarity 22.9%; Pred. No. 3.8;
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
 OY 1 MYVALPAMSPTTYLT---LLLSGLSGTQDCSPFQSPISDFAVKTRFLDYLLDYP 57
 DB 72 MGLSPGSGSPQRQVLRQKILPAMGVSS-----DHPFAPS-FRI-FNSLSS-----T 117
 OY 58 VIVASNLQDELQGLWRLVLAQRMMERIKTVYAGSKMGLLERVNTEIHFYTKCAFQPPP 117
 DB 118 CSWSSMDDE-----YMELEFMSQSQ-----QTAIGF-----P 146

```

OY 118 SCLRPVOTNISRLQETSEQLVAKP---WITRONFSKCLEL-QCQPDSSLTTPPMSPR 173
DB 147 SGLN-----SLISQIQEOPAKSPAGLSMRPSVRCISLMTSNSTTTPPKPE- 199
OY 174 LEATAPTA---POPPLLLLLLPVGLLLAAWCLHMORTRRRTPRGEQVPPVSPDOL 230
DB 200 ---TARDCKFRPEPP-----ASANCSPIOSKRNRCAAVKEKNCAPAPLSQ 242
OY 231 LLYEH 235
DB 243 VTISH 247

RESULT 9
DRL_RAT STANDARD: PRT; 910 AA.
AC 063474;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE PTK-3).
GN DRL1 OR EDDR1 OR PTK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA MEDLINE=94173920; PubMed=8127887;
RT Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid M.;
RT "Multiple tyrosine protein kinases in rat hippocampal neurons:
RT Isolation of Ptk-3, a receptor expressed in proliferative zones of
RT the developing brain.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
RL
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; L26525; AAA21089.1; -.
CC HSSP; P11362; IAGW.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR000421; FAS6_C.
CC InterPro; IPR002011; Receptor_tyr_kin_II.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00754; F5_F8_Type_C; 1.
CC Pfam; PF00069; F5_F8_Type_C; 1.
CC SMART; SM00231; FA58C; 1.
CC SMART; SM00219; TYRKC; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
CC PROSITE; PS01285; FA58C_1; 1.

```

```

DR PROSITE; PS01286; FA58C_2; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding.
FT SIGNAL 1 19
FT CHAIN 20 910
FT DOMAIN 20 413
FT TRANSMEM 414 440
FT DOMAIN 441 910
FT DOMAIN 32 186
FT 378 412
FT DOMAIN 473 598
FT DOMAIN 607 902
FT NP_BIND 613 621
FT BINDING 652 652
FT ACT_SITE 763 763
FT DISULFID 32 186
FT MOD_RES 510 510
FT MOD_RES 789 789
FT MOD_RES 793 793
FT MOD_RES 794 794
FT CARBOHYD 212 212
FT CARBOHYD 261 261
FT CARBOHYD 371 371
FT CARBOHYD 391 391
FT SEQUENCE 910 AA; 101164 MW; 7E7FFA1DCB029806 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 910;
Best Local Similarity 24.5%; Pred. No. 8.8; Mismatches 35; Indels 70; Gaps 9;
Matches 38; Conservative 12;

OY 143 PWITRONFSKCLELQCPDSSLTLP-PW---SPRPLEATA---PTAPDP----- 184
DB 356 PWLFFSLSTISDV-VNDSDFPPAPMWPPEPTNFSSLELEPRGQGVAKAECSPTA 414
OY 185 -----PLLLILLPVGLLLAAWCLHMOR-----TRRR-----T 214
DB 415 ILICGLVAIIILLILLIALLML---WRLHMRRLSKARVLEELTVHLSPGDTILLN 470
OY 215 PRGEQVPP-----VPSPDLLL 232
DB 471 NRPGPREPPYOEPRPAGTPTHSAPCVNPGSALL 505

RESULT 10
DRL_MOUSE STANDARD: PRT; 911 AA.
ID DRL_MOUSE
AC 003146;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE MPK-6).
GN DRL1 OR EDDR1 OR CAK OR MPK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL;
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RT coexpressed in breast tumor cell lines.";
RT Oncogene 12:1469-1477(1996).
RL
RN [2]
RN SEQUENCE OF 766-822 FROM N.A.
RN STRAIN=C57BL; TISSUE=Embryonic brain;
RC

```


RA Emerson P.C., Billinton A., Marshall F.H.;
 RT "The GABAB receptor interacts directly with the related transcription
 RT factors CREB2 and ATFx.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13967-13972(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kohraki J., Tanaka K.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 161-282 FROM N.A.
 RX MEDLINE-99303793; PubMed-10373550;
 RA Patel D., Melstreich M.L., Plon S.E.;
 RT "Human Cdc34 and Rad6b ubiquitin-conjugating enzymes target repressors
 RT of cyclic AMP-induced transcription for proteolysis.";
 RL Mol. Cell. Biol. 19:5001-5013(1999).
 CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
 CC (CONSENSUS: 5'GTGAGCT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY
 CC VIRAL AND CELLULAR PROMOTERS.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS WITH GABAB
 CC RECEPTOR.
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF305687; AAG22558.1; -;
 DR EMBL; AB021663; BAA78477.2; -;
 DR EMBL; AF101368; AAD28370.1; -;
 DR MIM; 606398; -;
 DR InterPro: IPR002637; Ham1p-like.
 DR InterPro: IPR001871; bZIP.
 DR Pfam: PF00170; bZIP.1.
 DR ProDom: PD004952; Ham1p-like; 1.
 DR SMART: SM00338; BRLZ; 1.
 DR PROSITE; PS00036; BZIP_BASIC; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Multigene family.
 FT DOMAIN 123 139 POLY-PRO.
 FT DOMAIN 186 194 POLY-PRO.
 FT DNA_BIND 210 230 BASIC MOTIF.
 FT DOMAIN 236 250 LEUCINE-ZIPPER (PROBABLE).
 FT CONFLICT 161 163 LLA->RHE (TN REF. 3).
 SQ SEQUENCE 282 AA; 30674 MW; DDB2P907CA0215A0 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 282;
 Best Local Similarity 29.9%; Pred. No. 3.4;
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;

QY 144 WIT-RONSRLQLCQCPDSSITLPPSPSP-LEATA----- 178
 DB 66 WTEKVDSTALPLPLPPTLPQP-SPYPPDLAASLLKELRQMEDFFLDAPLPP 124
 QY 179 ---PTAPQPLLLLLLPVGL-----LLLAAMCLH--WORTRRTPPGSQ 220
 DB 125 PSPPLPLPPLPAPAPSLPLSPFDLQPPVLDLIDLALTYCRNENQGEVGMPLPFPQ 184
 QY 221 VPPVSP 227
 DB 185 QPPPPSP 191

RESULT 14
 FCQN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE IGG receptor FCN large subunit p51 precursor (FCRN) (Neonatal FC
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).
 GN FCGRT OR FCRN.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX STRAIN-WISTAR;
 RC MEDLINE-89097257; PubMed-2911353;
 RA Simister N.E., Mostov K.E.;
 RT "An Fc receptor structurally related to MHC class I antigens.";
 RL Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epithelium;
 RX MEDLINE-90315866; PubMed-2534798;
 RA Simister N.E., Mostov K.E.;
 RT "Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RL major histocompatibility complex class I antigen homolog.";
 RN Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP MEDLINE-95059482; PubMed-7969498;
 RA Burneister W.P., Huber A.H., Bjorkman P.J.;
 RT "Crystal structure of the complex of rat neonatal Fc receptor with
 RL Fc.";
 RL Nature 372:379-383(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-98154319; PubMed-9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RL receptor.";
 RL Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
 CC LIKE HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X14323; CAA32503.1; -;
 DR EMBL; M35495; AAA41611.1; -;
 DR PIR; S02117; S02117.
 DR PIR; A37374; A37374.
 DR PDB; 1FRT; 14-FEB-95.
 DR PDB; 3FRU; 10-JUN-98.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IgG1; 1.

```

CC  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D26046; BAA05046.1; -.
DR  HSSP; P06601; IFLI.
DR  MGD; MGJ:99948; Atbfl.
DR  InterPro; IPR001356; Homeobox.
DR  InterPro; IPR003604; znf_U1.
DR  InterPro; IPR000822; znf-C2H2.
DR  Pfam; PF00006; homeobox. 4.
DR  Pfam; PF00096; zf-C2H2; 20.
DR  SMART; SM00389; HOX; 4.
DR  SMART; SM00355; znf-C2H2; 22.
DR  SMART; SM00451; znf_U1; 7.
DR  PROSITE; PS00027; HOMEBOX_1; 2.
DR  PROSITE; PS00071; HOMEBOX_2; 4.
DR  PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
DR  PROSITE; PS00157; ZINC_FINGER_C2H2_2; 9.
KW  transcription regulation; Activator; zinc-finger; Metal-binding;
KM  DNA-binding; Homeobox; Nuclear protein; Repeat.
FT  ZN_FING 79 103 C2H2-TYPE.
FT  ZN_FING 282 305 C2H2-TYPE.
FT  ZN_FING 641 664 C2H2-TYPE.
FT  ZN_FING 672 695 C2H2-TYPE.
FT  ZN_FING 727 751 C2H2-TYPE.
FT  ZN_FING 805 829 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 946 969 C2H2-TYPE (DEGENERATE).
FT  ZN_FING 985 1009 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 1041 1065 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 1089 1113 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 1233 1256 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 1262 1285 C2H2-TYPE.
FT  ZN_FING 1370 1395 C2H2-TYPE.
FT  ZN_FING 1411 1433 C2H2-TYPE.
FT  ZN_FING 1439 1462 C2H2-TYPE.
FT  ZN_FING 1555 1579 C2H2-TYPE.
FT  ZN_FING 1606 1630 C2H2-TYPE.
FT  ZN_FING 1990 2013 C2H2-TYPE.
FT  ZN_FING 2152 2211 HOMEBOX 1.
FT  DNA_BIND 2249 2308 HOMEBOX 2.
FT  DNA_BIND 2335 2358 C2H2-TYPE (ATYPICAL).
FT  ZN_FING 2539 2561 C2H2-TYPE.
FT  DNA_BIND 2650 2709 HOMEBOX 3.
FT  ZN_FING 2720 2743 C2H2-TYPE.
FT  DNA_BIND 2952 3011 HOMEBOX 4.
FT  ZN_FING 3032 3056 C2H2-TYPE.
FT  ZN_FING 3552 3576 C2H2-TYPE.
FT  ZN_FING 461 491 POLY-GLU.
FT  ZN_FING 771 785 POLY-ALA.
FT  ZN_FING 1314 1317 POLY-ALA.
FT  ZN_FING 1734 1748 POLY-GLN.
FT  ZN_FING 1794 1799 POLY-GLN.
FT  ZN_FING 1856 1863 POLY-GLN.
FT  ZN_FING 2044 2059 POLY-PRO.
FT  ZN_FING 2405 2408 POLY-ALA.
FT  ZN_FING 3216 3220 POLY-PRO.
FT  ZN_FING 3380 3409 POLY-GLN.
FT  ZN_FING 3412 3420 POLY-GLN.
FT  ZN_FING 3534 3550 POLY-GLY.
FT  ZN_FING 3620 3623 POLY-PRO.
FT  ZN_FING 3659 3662 POLY-SER.
SO  SEQUENCE 3726 AA; 406567 MW; 913ACE568A72C98 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 3726;
Best Local Similarity 21.6%; Pred. No. 71;
Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;

OY 29 DCSQHSPLSSDPAVKYKIRELSYLLQDPYVVAANLDEE--LGGGMRLYLAQRMERT 86
DB 3033 ECTLCGKTKTSARLSVDHIFISQOHISKYKNDITSLDLKREKREYDPATVROLMAQQLDRI 3092
OY 87 KTV-----ASAKMOGL-----LERYNTEIHVYTCARQ--PP-----PSCLEFVQTN 126

```

```

DB 3093 KKANVGLAAQQQGFMDNAPLQALMLP---TTPALQGIPIVLLPGINRSLPGFTPAN 3149
QY 127 ISRLQETSEQLVLRKFWITRQNFSCRLQCCQPSSTLPFPW-----S 170
DB 3150 TA-----LTSRPR-----NLMQLP-STYTPSGCLPTSGLPKPKSSASLSS 3188
QY 171 PRELEATAPAPAPPLLLLLLPLVGLLLAAAMCLHMORTRRRTTRPGEQVPP----- 223
DB 3189 PTPAQATMAMAPQP-----PQOPQOPVPOQPPPPPAQAQ 3224
QY 224 VPSPQ 228
DB 3225 IPAPQ 3229

RESULT 16
MNT_HUMAN STANDARD; PRT; 582 AA.
AC 09583;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAX binding protein MNT (ROX protein) (MYC antagonist MNT).
GN MNT OR ROX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=97337566; PubMed=9184233;
RA Meroni G., Raymond A., Alcalay M., Borsani G., Tanigami A.,
RA Tonlorenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.,
RA Brent R., Ballabio A., Carrozzo R.;
RT "Rox, a novel bHLHZip protein expressed in quiescent cells that
RT heterodimerizes with Max, binds a non-canonical E box and acts as a
RT transcriptional repressor.";
RL EMO J. 16:2892-2906(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98260677; PubMed=9598315;
RA Nigro C.L., Venesio T., Raymond A., Meroni G., Alberici P.,
RA Calanca S., Enrico F., Stack M., Ledbetter D.H., Liscia D.S.,
RA Ballabio A., Carrozzo R.;
RT "The human ROX gene: genomic structure and mutation analysis in human
RT breast tumors.";
RL Genomics 49:275-282(1998).
CC -1- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
CC TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE
CC 5'-CAGCG-3' AND, WITH HIGHER AFFINITY, TO 5'-CAGCG-3'.
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X96401; CAA65265.1; -
DR EMBL: Y13440; CAA73851.1; -
DR EMBL: Y13441; CAA73851.1; JOINED.
DR EMBL: Y13442; CAA73851.1; JOINED.
DR EMBL: Y13443; CAA73851.1; JOINED.
DR EMBL: Y13444; CAA73851.1; JOINED.
DR HSSP: P25912; IHL0.

```

```

DR TRANSFAC; T03268; -.
DR MIM: 603039; -.
DR InterPro: IPR003015; HLH_MYC.
DR InterPro: IPR001092; HLH_dim.
DR Pfam: PF00010; HLH_1.
DR SMART: SM00353; HLH_1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
FT DNA_BIND 222 233
FT DOMAIN 234 270
FT DOMAIN 271 299
SQ SEQUENCE 582 AA; 62299 MW; 06AC320D79BF18A0 CRC64;

Query Match 6.8%; Score 84; DB 1; Length 582;
Best Local Similarity 21.1%; Pred. No. 9.4;
Matches 61; Conservative 35; Mismatches 89; Indels 104; Gaps 13;

QY 4 LAPASPTTYLLLLLLLS-----GLSTQDCSFQHSPISSDFAKIRELSDY 51
DB 186 LAPQPPPTLTGLKLAPEYKSSQKKRPGIGTREV---HNKLEKNRAHLKEGFEI 242
QY 52 LLDYPTVYASNLQDEELCGLMRLVLAQRMERIKTVAGSKQGLLERVNTEIHFYTKC 111
DB 243 LKRNIP-----NVDDKK-TSNLSVLTALRYIQSLKR-KEKEYHEMERLARE-----KI 290
QY 112 APQPPRSCLRFVQNTNSRLQETSEQLVLRKFWITRQNFSCRLQCCQPSSTLPFPW----- 161
DB 291 A-----TQRLAEKLHELSSQ-----WMDVEIDRYLQGTQGPEDDQASTSTAS 333
QY 162 -----STLPPP-WSPRELEATAPAPQPLLLL 189
DB 334 EGEDNIDEMEDRAGLGPRKLSHRPOPELLKSTLPSPSTPAPLV---PPNPRH- 385
QY 190 LILPVGLLLAAAMCLHMORTRRRTTRPGEQVPP-----VPSPQDIL 231
DB 386 ---PNSVALPRHLRYQQQPOQKTRLPAPPPPPAPAAQGLVPRAPHLY 431

RESULT 17
YF48_HUMAN STANDARD; PRT; 732 AA.
AC 09HCW4; Q9H975;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA1548.
GN KIAA1548.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai I., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
RT "NEO human cDNA sequencing project.";
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 188-732 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

```

CC      The European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC
CC      -----
DR      EMBL; AK023019; BAB14360.1; -
DR      EMBL; AB046768; BAB13374.1; -
DR      InterPro; IPR000299; Band_4.1.
DR      Pfam; PF00373; Band_41; 1.
DR      PRINTS; PR00935; BAND41.
DR      SMART; SMO0295; BA1; 1.
DR      PROSITE; PS00660; BAND_41.1; 1.
DR      PROSITE; PS00661; BAND_41.2; 1.
DR      PROSITE; PS50057; BAND_41.3; 1.
DR      Hypothetical protein; Cytoskeleton.
KW      DOMAIN 40 235 BAND 4.1-LIKE.
FT      DOMAIN 40 235
FT      CONFLICT 669 732 SGANSNGIACGEMILNKGKNGKNDGISLSPAPFLVDAY
FT      TSSGIIAEAVLAKOCLITTEL -> LMSHGGRSCEAE
FT      VETSD (IN REF. 1).
SQ      SEQUENCE 732 AA; 81758 MW; 7605DB8C809E761 CRC64;

Query Match 6.8%; Score 84; DB 1; Length 732;
Best Local Similarity 24.9%; Pred. No. 12;
Matches 42; Conservative 23; Mismatches 50; Indels 54; Gaps 8;

QY      11 TTYLLLLLLSSSLGSTDCCSFQHSPISSDFAVKI-----RELSDVLLDDYPVTAASN- 63
      |||:|:| ||| ||| ||| |||:|:| ||| |||:|:|
Db      135 TRYFLVQLKQDILSKLDPCF-----DPAVGLAANVLAELGDVDLAHSPELVSE 187

QY      64 -----LDDELGGSLMKLVLAQRMM-RLKYTAGSGMGL-----LEKYNELIHPV----- 108
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      188 RVPVPIQTEH-----ELALFEKMKKEKQGPAPQAFETNLNKAWEVGVDMVHVARQD 242

QY      109 -----TKCA--FQPPSCIRFEVQTNIRLLQETSEQ 137
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      243 NDVSLGLTPGVLFEGDTRIGLFEWPKRTRTRLDFEKNKRLTLVVEDDQ 291

RESULT 18
ID      2282_HUMAN STANDARD; PRT; 671 AA.
AC      G9UDVT; 043691;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Zinc finger protein 282 (HIV-1 USRE binding protein 1) (HUB-1).
GS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE FROM N.A.
RX      MEDLINE=98060901; PubMed=9396811;
RA      Okumura K., Sakaguchi G., Naito K., Tamura T., Igarashi H.;
RT      "HUB1, a novel kruppel type zinc finger protein, represses the human T
RT      cell leukemia virus type I long terminal repeat-mediated expression.";
RL      Nucleic Acids Res. 25:5025-5032(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Bemis G., Langston Y., Tucci S.;
RL      Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: BINDS TO THE US REPRESSIVE ELEMENT (USRE) OF THE HUMAN T
CC      CELL LEUKEMIA VIRUS TYPE I LONG TERMINAL REPEAT. IT RECOGNIZES THE
CC      TCCACCCC SQDQDCE AS A CORE MOTIF AND EXERTS A STRONG REPRESSIVE
CC      EFFECT ON HTLV-I LTR-MEDIATED EXPRESSION.
CC      -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC      -1- TISSUE SPECIFICITY: UNIDIOUS.
CC      -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C/2H2-TYPE ZINC-
CC      FINGER PROTEINS.
CC      -1- SIMILARITY: CONTAINS 1 KRAB DOMAIN.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on just
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.slb.ch/annouce/slb.ch).
CC or send an email to license@slb.ch).
CC -----
DR EMBL: D36612; BAA24380.1; ALT_INIT.
DR EMBL: AC004890; AAD45825.1; ALT_INIT.
DR HSSP: P08047; 1SP2.
DR MIM: 603397; -.
DR InterPro: IPR001909; KRA6.
DR InterPro: IPR000822; Znf-C2H2.
DR Pfam: PF01352; KRA6; 1.
DR Pfam: PF00096; Zf-C2H2; 5.
DR SMART: SM00349; KRA6; 1.
DR SMART: SM00355; Znf-C2H2; 5.
DR PROSITE: PSS0805; KRA6; 1.
DR PROSITE: PSS0028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE: PSS0157; ZINC_FINGER_C2H2_2; 5.
DR Transcription regulation, DNA-binding; Zinc-finger; Metal-binding;
KM Nucleic protein, Repeat; Repressor.
KM KRA6.
FT DOMAIN 198 271
FT ZN_FING 518 552 ZINC_FINGERS.
FT ZN_FING 518 540 C2H2-TYPE.
FT ZN_FING 546 568 C2H2-TYPE.
FT ZN_FING 574 596 C2H2-TYPE.
FT ZN_FING 602 624 C2H2-TYPE.
FT ZN_FING 630 652 C2H2-TYPE.
FT CONFLICT 35 35 Q -> E (IN REF. 2).
FT CONFLICT 317 317 T -> V (IN REF. 2).
FT CONFLICT 414 414 R -> P (IN REF. 2).
SQ SEQUENCE 671 AA; 74353 MW; 3E16D325576E5FF5 CRC64;

Query Match 6.7%; Score 83.5; DB 1; Length 671;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 43; Conservative 20; Mismatches 51; Indels 75; Gaps 10.

OY 65 QDEELGGLRWLYLAQRMER---LKVAGSKM--GGLEPRVTEIHFWYTKCAFQPPS 118
DB 294 REDILG-----VRGGRGLEERAIPIRESITDPSIAQDLRSIKOEHR--QCWWDQDL 344
OY 119 CLRFRQINISRLGENSEQVLAK-----PWTRONFNSCLETQCPDSSTL 165
DB 345 ADRIQLPND-----PNSSELISAHDLISWIKOEBOPIYWGGRDSDMDGELGDSPPSSLL 398
OY 166 ----PPWSPPLPAPAPAPOPPLLILLILDPVGLILLAAACLMHQRTRRRPRREGQV 221
DB 399 WKNWPP-----APQPOP-----GRQPOP--QL 421
OY 222 PPVSPQDL 230
DB 422 QSQPQPSL 430

RESULT 19
VKGC_HUMAN STANDARD; PRT; 758 AA.
AC P38435; O14415;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin K-dependent gamma-carboxylase (PC 6.4.-.-) (Gamma-g)utanyl
DE carboxylase).
DE GN GCCK OR GC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE-92086858; PubMed-1749935;
 RA Wu S.-M., Cheung W.-F., Frazier D., Stafford D.W.;
 RT "Cloning and expression of the cDNA for human gamma-glutamyl
 RT carboxylase";
 RL Science 254:1634-1636(1991).
 RP SEQUENCE FROM N.A.
 RA Wu S.-M., Chu K., High K.A., Stafford D.W., Solera J.;
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Yung L., Lipsky J.U.;
 RL Submitted (Mar-1996) to the EMBL/GenBank/DBJ databases.
 RX MEDLINE-9906171; PubMed-9845520;
 RA Brenner B., Sanchez-Vega B., Wu S.M., Lanir N., Stafford D.W.,
 RA Solera J.;
 RT "A missense mutation in gamma-glutamyl carboxylase gene causes
 RT combined deficiency of all vitamin K-dependent blood coagulation
 RT factors";
 RL Blood 92:4554-4559(1998).
 CC -1- FUNCTION: VITAMIN K-DEPENDENT CARBOXYLATION OF MULTIPLE AMINO-
 CC TERMINAL GLUTAMIC ACID RESIDUES IN VARIOUS PROTEINS, IT CONVERTS
 CC GLUTAMATE RESIDUES TO GAMMA-CARBOXYGLUTAMATE.
 CC -1- SUBUNIT: MAY FORM A HOMODIMER (PROBABLE).
 CC -1- DISEASE: DEFECTS IN GGCC ARE A CAUSE OF COMBINED DEFICIENCY OF ALL
 CC VITAMIN K-DEPENDENT PROCOAGULANTS AND ANTICOAGULANTS; ALSO KNOWN
 CC AS MULTIPLE COAGULATION FACTOR DEFICIENCY III (MCPD3).
 CC -1- SIMILARITY: SOME, TO PLANT AND MAMMALIAN LIPOXYGENASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M81592; AAA58643.1; -;
 DR EMBL: U65896; AAB39832.1; -;
 DR EMBL: L17128; AAA91834.1; -;
 DR MIM: 137167; -;
 DR MIM: 277450; -;
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR Ligase; Polymorphism; Disease mutation.
 FT VARIANT 325 Q -> R.
 FT /FTID=VAR_005780.
 FT VARIANT 394 394 L -> R (IN MCPD3).
 FT /FTID=VAR_005781.
 FT CONFLICT 400 400 D -> N (IN REF. 3).
 FT SEQUENCE 758 AA; 87532 MW; 2CDDC365085569E7 CRC64;
 SQ

DB 630 -----ETGPLEPQLP-LEGVKGGEPTPLVQFTL 660
 RESULT 20
 ID MM1_HUMAN STANDARD; PRT; 488 AA.
 AC P24347;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Stromelysin-3 precursor (EC 3.4.24.-) (Matrix metalloproteinase-11)
 DE (MMP-11) (ST3) (SL-3).
 GN MMP11 OR STMT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91080920; PubMed-1701851;
 RA Basset P., Bellocq J.P., Wolf C., Stoll I., Rutin P., Lmacher J.M.,
 RA Podhajcer O.U., Chenard M.P., Rio M.C., Chambon P.;
 RT "A novel metalloproteinase gene specifically expressed in stromal
 RT cells of breast carcinomas";
 RL Nature 348:699-704(1990).
 RN [2]
 RP SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE-9536471; PubMed-7657606;
 RA Anglard P., Meiot T., Guerin E., Basset P.;
 RT "Structure and promoter characterization of the human Stromelysin-3
 RT gene";
 RL J. Biol. Chem. 270:20337-20344(1995).
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE PROGRESSION OF
 CC EPITHELIAL MALIGNANCIES.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN STROMAL CELLS OF
 CC BREAST CARCINOMAS.
 CC -1- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
 CC METALLOPROTEASE). ALSO KNOWN AS MATRILIN SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X57766; CAA40918.1; ALT-SEQ.
 DR EMBL: X84664; CAA59150.1; -;
 DR PIR: S13423; S13423.
 DR HSSP: P08254; 10SN.
 DR MEROPS: M10.007; -;
 DR MIM: 185261; -;
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Matrxin.
 DR InterPro: IPR000130; zn_MTPeptide.
 DR Pfam: PF00045; hemopexin; 4.
 DR PRINTS: PR00138; MATRILIN.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZnMc; 1.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium;
 KW Collagen degradation; Extracellular matrix; Signal.
 FT SIGNAL 1 31
 FT PROPEP 32 97 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 98 488 STROMELYSIN-3.
 FT DOMAIN 291 483 HEMOPEXIN-LIKE.
 FT SITE 80 80 CYSTEINE SWITCH (BY SIMILARITY).
 FT

RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases
 CC -! FUNCTION: COMPONENT OF THE SARCOGLYCIN COMPLEX, A SUBCOMPLEX OF
 CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
 CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
 CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMMAL
 CC (POTENTIAL).
 CC -! SIMILARITY: BELONGS TO THE SARCOGLYCIN ALPHA/EPSILON FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB024920; BAA83491.1; -
 DR EMBL: AF064081; AAC33447.1; -
 DR MGI: 894698; Sgca.
 KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 1 23
 FT DOMAIN 24 387
 FT TRANSMEM 24 293
 FT DOMAIN 294 314
 FT DOMAIN 315 387
 FT CARBOHYD 174 174
 FT CARBOHYD 246 246
 FT SEQUENCE 387 AA; 43286 MW; 7C3D98A853D04591 CRC64;
 SO
 Query Match 6.5%; Score 81; DB 1; Length 387;
 Best Local Similarity 22.7%; Pred. No. 11;
 Matches 69; Conservative 26; Mismatches 99; Indels 110; Gaps 14;
 Oy 11 TTYLLLLLLSSGSGGOCSPFHSPISSDFAKITRELSDYLDQPYPTVASNDELIC 70
 Db 115 TTRRRLRLIG-----DEGRPLRYQAEFLRSHDEEVL-----PTTPANRL--TAL 161
 Oy 71 GGLN-----RLVLAQRMERLKTVAASKMOGLLERYNEIHFVT-----K 110
 Db 162 GILTEPELQDLNITSALDRGGRVPLPIEGRKEGVYIKVGSATPSTCLKWASPSYAR 221
 Oy 111 CAFQRPPE--SC-----LRFVQTNISRLQETSRLVLAQKWTIRQNFSCLELCOPD 161
 Db 222 CAQCGPRLSCYDTLAPHFVPMCVNLSYDKSVPELD-----EYTPPGD 266
 Oy 162 SSTLPWPSPRLPEAT-----APYAPQRPRLLLLLPVGLLLAAMC----- 204
 Db 267 GILHDPFPCPPEATDRDFLDALVTLLVPLLVALL--TLLAYIMCFRRREGRLKRD 323
 Oy 205 -----LHMQRTRRRPRP-----GEQVPR-VPSPO-DL 231
 Db 324 MATSDIQMFHHSIHGTEELRQMAASREVPRLSLTFMENVRTGERLPRVDSNQMPLI 383
 Oy 232 LVEH 235
 Db 384 LDQH 387
 RESULT 25
 EPC_HUMAN STANDARD; PRT; 428 AA.
 AC P01854;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig epsilon chain C region.
 GN IGHE
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN {1}
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83168897; PubMed-6300763;
 RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarrashi K.,
 RA Kiyuchi M., Sugino Y., Nishida Y., Honjo T.;
 RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
 RT epsilon chain cDNA.";
 RL Nucleic Acids Res. 11:719-726(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83001945; PubMed-6288268;
 RA Max E.E., Batley J., Ney R., Kirsch I.R., Leder P.;
 RT "Duplication and deletion in the human immunoglobulin epsilon genes.";
 RL Cell 29:691-699(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84236029; PubMed-6234164;
 RA Flanagan J.G., Rabbits T.H.;
 RT "The sequence of a human immunoglobulin epsilon heavy chain constant
 RT region gene and evidence for three non-allelic genes.";
 RL EMBO J. 1:655-660(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84207910; PubMed-6327276;
 RA Ueda S., Nakai S., Nishida Y., Hiseajima H., Honjo T.;
 RT "Long terminal repeat-like elements flank a human immunoglobulin
 RT epsilon pseudogene that lacks introns.";
 RL EMBO J. 1:1539-1544(1982).
 RN [5]
 RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
 RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RL (in) Bach M.K. (eds.);
 RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 RN [6]
 RP SEQUENCE OF 1-40: 68-114 AND 427-428 FROM N.A.
 RX MEDLINE-83065234; PubMed-6815656;
 RA Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 RN [7]
 RP 3D-STRUCTURE MODELING.
 RA Padlan E.A., Davies D.R.;
 RT "A model of the Fc- of immunoglobulin E.";
 RL Submitted (JUL-1993) to the PDB data bank.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L00022; AAB59424.1; ALU_INTT.
 DR PIR: A02142; EHHU.
 DR PIR: A22771; A22771.
 DR PIR: A23195; A23195.
 DR PDB: 1IGE; 15-JUL-92.
 DR MIM: 147180; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00407; Ig-c1; 4.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DISULFID 14 14
 FT DISULFID 15 105
 FT DISULFID 29 85
 FT DISULFID 121 121
 INTERCHAIN (WITH A LIGHT CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).

FT	DISULFID	135	193	
FT	DISULFID	209	209	
FT	DISULFID	239	299	
FT	DISULFID	345	405	
FT	CARBOHYD	21	21	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	146	146	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	252	252	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	275	275	N-LINKED (GLCNAC. . .)
FT	VARIANT	359	359	W -> L (IN REF. 2, POSSIBLY DUE TO POLYMORPHISM).

INTERCHAIN (WITH A HEAVY CHAIN).

SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64; /FTIG-VAR_003885.

Query Match 6.5%; Score 81; DB 1; Length 428;

Best Local Similarity 21.6%; Pred.No.12; Mismatches 83; Indels 70; Gaps 8;

Matches 48; Conservative 21; Mismatches 83; Indels 70; Gaps 8;

QY	2	TVLAPANSPTT---	YLLILLSSGLSGTQ--DCSFQHSPISSDF-----	41
DB	52	TMTLPATTLTSLGHTATISLTVSGAMAKQMFRCRAVAHTPSSTDWVDNKTFSVCSRDFTF	111	
QY	42	-----	AVKIRELSDYLDYPTVANSNLQDEEL	69
DB	112	PTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDOVMVDLSTASTQEGEL	171	
QY	70	CGGLMRVLVAQR-WMERLKTIVAGSKMQGLIERVNTIEHFVKCAFQPPSCLEFVQTNIS	128	
DB	172	ASTQSEILTSOKHMLSDRTYTCQVYQGHTEFEDSTK-----	KCADSNP-----RGYSAYLS	222
QY	129	RLLOETSEQLVALKPMWTRONFRCLELQCCQPDSTLPPWS	170	
DB	223	R--PSPFDLFIKRSPTIT-----	CLVVDLAPSKGTVNLWTS	256

Search completed: August 6, 2002, 09:46:19
Job time: 400 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:04 ; Search time 47.12 Seconds

(without alignments)
862.772 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLAPAMSPRTYLLILL.....RPEQVPPVSPDILLVH 235

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

1: SP:archae:.*
2: SP:bacteria:.*
3: SP:fungi:.*
4: SP:human:.*
5: SP:invertebrate:.*
6: SP:mammal:.*
7: SP:mhc:.*
8: SP:organelle:.*
9: SP:phage:.*
10: SP:plant:.*
11: SP:rodent:.*
12: SP:virus:.*
13: SP:vertebrate:.*
14: SP:unclassified:.*
15: SP:virus:.*
16: SP:bacteriap:.*
17: SP:archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	6 Q9MZV0	Q9mzv0 canis famli
2	894.5	72.0	291	6 Q9MZU9	Q9mzu9 felis silve
3	840	67.6	292	6 Q9GKE0	Q9gke0 bos taurus
4	746	60.1	274	6 Q9GKD9	Q9gkd9 bos taurus
5	602.5	48.5	172	11 Q61104	Q61104 mus musculu
6	112.5	9.1	579	10 Q9LGS8	Q9lgs8 oryza sativ
7	104.5	8.4	668	5 Q9GY11	Q9gy11 leishmania
8	102.5	8.3	648	5 Q9GY33	Q9gy33 leishmania
9	98.5	7.9	345	5 Q9N753	Q9n753 leishmania
10	95.5	7.7	1240	12 Q9DWH8	Q9dwh8 rat cytoleg
11	93.5	7.5	658	10 Q9C5F0	Q9c5f0 arabidopsis
12	93	7.5	1217	5 Q17889	Q17889 caenorhabdi
13	92.5	7.4	560	5 Q9GYA1	Q9gya1 leishmania
14	92	7.4	251	4 Q9HAD2	Q9had2 homo sapien
15	90.5	7.3	536	4 Q9GYA0	Q9gya0 leishmania
16	90.5	7.3	660	5 Q9GY15	Q9gy15 leishmania

17	90.5	7.3	5120	13 Q9PU36	Q9pu36 gallus gall
18	89.5	7.2	474	5 Q17610	Q17610 caenorhabdi
19	88.5	7.1	270	4 Q9UMT1	Q9umt1 homo sapien
20	88.5	7.1	404	10 Q9AMJ4	Q9amj4 oryza sativ
21	88.5	7.1	1267	10 Q9AJM3	Q9ajm3 oryza sativ
22	88.5	7.1	1386	4 Q75064	Q75064 homo sapien
23	88	7.1	250	6 Q9GKE2	Q9gke2 sus scrofa
24	88	7.1	675	11 Q9DBT2	Q9dbt2 mus musculu
25	88	7.1	753	12 Q56971	Q56971 kenedya ye
26	87.5	7.0	470	10 Q9JUI1	Q9ju11 arabidopsis
27	87.5	7.0	946	10 Q22015	Q22015 cyllindroche
28	87	7.0	510	5 Q44018	Q44018 leishmania
29	86.5	7.0	299	6 Q9TTF9	Q9ttf9 bos taurus
30	86	6.9	255	11 Q9DJ33	Q9dj33 mus musculu
31	86	6.9	299	12 Q84647	Q84647 paramecium
32	86	6.9	706	5 Q23600	Q23600 caenorhabdi
33	86	6.9	911	11 Q35407	Q35407 mus musculu
34	85.5	6.9	795	5 Q95U02	Q95u02 toxoplasma
35	85	6.8	282	4 Q9BSA1	Q9bsa1 homo sapien
36	85	6.8	289	16 Q9A3K1	Q9a3k1 caulobacter
37	85	6.8	413	11 Q9JMM1	Q9jmm1 mus musculu
38	85	6.8	1217	4 Q9P2D0	Q9p2d0 homo sapien
39	84.5	6.8	780	13 Q9OX41	Q9ox41 brachydanio
40	84.5	6.8	932	11 Q99JH4	Q99jh4 mus musculu
41	84.5	6.8	1134	4 Q96JH1	Q96jh1 homo sapien
42	84	6.8	220	4 Q96030	Q96030 homo sapien
43	84	6.8	224	6 Q19031	Q19031 ovis aries
44	84	6.8	263	12 Q36417	Q36417 alcelaphine
45	84	6.8	543	6 Q95NM2	Q95nm2 oryctolagus
46	84	6.8	567	11 Q99J43	Q99j43 mus musculu
47	84	6.8	1234	11 Q9R044	Q9r044 rattus norv
48	84	6.8	1252	11 Q9QXX7	Q9qxx7 rattus norv
49	84	6.8	1252	11 Q9JIX2	Q9jix2 rattus norv
50	83.5	6.7	199	16 Q9RZL3	Q9rzt3 deinococcus

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	294 AA.
Q9MZV0	Q9MZV0			
AC	Q9MZV0			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)			
DE	FLR3 LIGAND.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20358731; PubMed=10902925;			
RA	Yang S., Sim G.K.;			
RT	"Molecular cloning of canine and feline flr3 ligand reveals high			
RT	degree of similarity to the human and mouse homologue but uniquely			
RT	long cytoplasmic domain."			
RL	DNA Seq. 11:163-166(2000).			
DR	EMBL; AF15148; AAF87088.1; -			
SO	SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;			

Query Match	72.1%;	Score 895.5;	DB 6;	Length 294;
Best Local Similarity	77.1%;	Pred. No. 7.9e-82;		
Matches 182;	Conservative 12;	Mismatches 35;	Indels 7;	Gaps 3;
QY	1	MTVLAPAMSPRTYLLILLSSGSGTQDSFQHSPTSSDPFAVKIRELSYLLQDPVTV	60	
DB	1	MTVLAPAMSPRTYLLILLSSGSGTQDSFQHSPTSSDPFAVKIRELSYLLQDPVTV	60	
QY	61	ASNDDELICGGLRWLVLAORWMLRTVAGSKMGLLEVNNEIHFVTCAPQPPSC	120	

Db 61 ASNLQDELGCAGFWRLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 120
 QY 121 RFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180
 Db 121 RFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180
 QY 181 APQAP--LLLLLLPVGILLAAACLMW-ORTRRRTPRGEGVPPVS-----POD 229
 Db 181 APQAPRLLLLLLPPVALLLMSTAMCLHWRRRRRRRSPYGEQRTLRPSERSHLPED 236

RESULT 2
 Q9MZ09 PRELIMINARY; PRT; 291 AA.
 AC Q9MZ09;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE FLT3 LIGAND.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF15149; AAF87089.1; -
 SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;
 Best Local Similarity 80.5%; Pred. No. 9,8e-82;
 Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;
 QY 1 MTVLAPAMSPPT--YLLLLLLLSGLSGTQDCSFQHPSPSSDPFAVKIRELSDYLLQDYPVT 60
 Db 1 MYTLAPAMSPPTSLLLLLLLSPGLRSGPDCSFHSPISSTFKYTKIKLSLDYLLQDYPVT 60
 QY 61 ASNLQDELGCGLMRVLVAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPPSC 120
 Db 61 ASNLQDELGCGLMRVLVAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPPSC 120
 QY 121 RFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180
 Db 121 RFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180
 QY 181 APQAP--LLLLLLPVGILLAAACLMW-ORTRRRTPRGEGVPPVS-----POD 229
 Db 181 APQAPRLLLLLLPPVALLLMSTAMCLHWRRRRRRRSPYGEQRTLRPSERSHLPED 221

RESULT 3
 Q9GKE0 PRELIMINARY; PRT; 292 AA.
 AC Q9GKE0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE FLT3 LIGAND ISOFORM-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF99322.1; -
 DR InterPro; IPR004213; flt3_1lg.
 DR Pfam; PF02947; flt3_1lg; 1.
 SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;
 Best Local Similarity 76.3%; Pred. No. 2,9e-76;
 Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;
 QY 1 MTVLAPAMSPPT--YLLLLLLLSGLSGTQDCSFQHPSPSSDPFAVKIRELSDYLLQDYPVT 59
 Db 1 MTVLAPAMSPPTSLLLLLLLSPGLRSGPDCSFHSPISSTFKYTKIKLSLDYLLQDYPVT 60
 QY 60 VASNLQDELGCGLMRVLVAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPPSC 119
 Db 61 VASNLQDELGCAGFWRLVLAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPLPSCL 120
 QY 120 LRFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 179
 Db 121 LRFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180
 QY 180 TAPQPP--LLLLLLPVGILLAAACLMW-ORTRRRTPRGEGVPPVS-----POD 220
 Db 181 PEGQSPRLLLLLLPPVALLLMSTAMCLHWRRRRRRRSPYGEQRTLRPSERSHLPED 224

RESULT 4
 Q9GKD9 PRELIMINARY; PRT; 274 AA.
 AC Q9GKD9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE FLT3 LIGAND ISOFORM-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Mwangi W., Brown W.C., Palmer G.H.;
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282986; AAF99323.1; -
 DR InterPro; IPR004213; flt3_1lg.
 DR Pfam; PF02947; flt3_1lg; 1.
 SQ SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match 60.1%; Score 746; DB 6; Length 274;
 Best Local Similarity 69.6%; Pred. No. 7,5e-67;
 Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;
 QY 1 MTVLAPAMSPPT--YLLLLLLLSGLSGTQDCSFQHPSPSSDPFAVKIRELSDYLLQDYPVT 59
 Db 1 MTVLAPAMSPPTSLLLLLLLSPGLRSGPDCSFHSPISSTFKYTKIKLSLDYLLQDYPVT 60
 QY 60 VASNLQDELGCGLMRVLVAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPPSC 119
 Db 61 VASNLQDELGCAGFWRLVLAQRMWRLKTVAGSKMGLERVNTTEIHFTVFCAPQPLPSCL 120
 QY 120 LRFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 179
 Db 121 LRFVQNTISRLQETSQDLVLAQRMWRLQAVASQMLLEAVNTEIHFTVFCAPQPLPSCL 180

QY 180 TAPQPP---LILLILLPVGLLLAAWCMQWRRTRRTPPQEG 220
Db 163 PGPSPLLLLLLLLPVALLLATATWCLCFWRRRRTTYPGGER 206

RESULT 5
061104 PRELIMINARY; PRT; 172 AA.

AC 061104;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN FLT3L LIGAND, T169 FORM.
CN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Matson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,
RT "Flt3 ligand: expression, genomic organization, alternatively spliced
RT forms and processing";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U44024; AAA93305.1; -.
DR MGD: MGI:95560; Flt3l.
DR InterPro: IPR004213; flt3_119.
DR Pfam: PF02947; flt3_119; 1.
SQ SEQUENCE 172 AA; 19465 MW; 04F0A010171E3384 CRC64;

Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 1.e-52;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;

QY 1 MTVALPAMSP-TTYVLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLDDYPTV 59
Db 1 MTVALPAMSPSSLLLLLLSPCLRTGTPCYSHSPISNFKVRELTDLTKDVPVT 60
QY 60 VASNIODELGGIMRLVLAQRMWERLKTAVAGSKMGLERVTETHEFTKCAFOPPSP 119
Db 61 VAVNLQDEKCKALMSLELAQRMWIEQLKTAVAGSKMGLERVTETHEFTKCAFOPP 120
QY 120 LRFVQTINISRLQETSEQLVAKFWITR--QNTSRCLQLCCQPDSSSTL 165
Db 121 LRFVQTINISHLKDTQTLALKFCIGKACQNFSCRLEVCQCPDRVSL 168

RESULT 6
09LGG8 PRELIMINARY; PRT; 579 AA.

AC 09LGG8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN PUTATIVE EXTENSIN-LIKE PROTEIN.
GN P0406H10.6 OR C01174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RL clone: P0406H10.";
RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone: C01174.D05.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF002524; BAB07956.1; -.
DR EMBL: AF003118; BAB33013.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR000504; RRM.
DR Pfam: PF00560; LRR; 6.
DR PRINTS: PR01217; PRICHEXTENSIN.
DR SMART: SM00370; LRR; 5.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;
Best Local Similarity 23.7%; Pred. No. 0.0077;
Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

QY 17 LILLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLDDYPTVASNIODEELCGGLMRL 76
Db 244 LILLINGLS-----SCLPPEVGM-LREVTVF-----DVSFNRLAGPLPSA 282
QY 77 VLAQRMWERLKTAVAGSKMGLERVTETHEFTKCAFO-----PPSCLRPV-----QT 125
Db 283 VAGMKRVEQL-DVAHNLGLGALPQAVCEL.PRLKNFTFVNFETGPPSCAHAVPYGRR 341
QY 126 NI--SRLQETSEQLVAKFWITRQNFNR---CLELQCPDSSSTLPPWSPRLPEATAP 179
Db 342 NCLPNRPAQRTLRQCAAF-----FARPPVNCARFQCKPVPALPPSPSPSP--SPPP 391
QY 180 TAPQPLLLLLLPVGLLLAAWCMQWRRTRRTPPQEGVPPVSP 227
Db 392 PPSPPP-----SPPPSPSPSPSP 411

RESULT 7
09GY11 PRELIMINARY; PRT; 668 AA.

AC 09GY11;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN PROBABLE SURFACE ANTIGEN P2.
GN IM12.156.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL390114; CAC02038.2; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002965; P-rich_extensn.
DR Pfam: PF00560; LRR; 8.
DR PRINTS: PR01217; PRICHEXTENSIN.
DR SMART: SM00181; EGF; 1.
SQ SEQUENCE 668 AA; 70725 MW; CEB3ECCABCA90C94 CRC64;

Query Match 8.4%; Score 104.5; DB 5; Length 668;
Best Local Similarity 26.6%; Pred. No. 0.058;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;
QY 4 LAPAMSPTTYVLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLDDYPTVASN 63

```
Db 149 LPPWSSMNPINQTLQVRLKLSGT-----LPADMS-SLKSLSNVLEDMPT----- 194
OY 64 LQDEELCGGLMRVLAQRMMERLKTAVAGSKMGGLEERVNEIHVTCARQPP-----S 118
Db 195 -----GL-----LPPBW-----GSLERIQQLVLRKLTGTPLPQWSPMK 229
OY 119 CLAREVO---TWISRLQ-----ETSEQLVALKP-WITRONFSRCLELQCP 160
Db 230 ALRRLTLDTGTLSTGLPQWMSAMASVISLNLEGTVEGTLPPKMSMSRL-QTLNLRRTK 288
OY 161 DSSLTPPPWSPR-----PLEATAPAPQPP-----LILLILPVGLL--LLAAAV 203
Db 289 VSGTLPPWSSMGLANLQSLTGVSTLPQWSSMKRLTQLLTLDTLLSGTLPAEW 345

RESULT 8
OY 09GY33 PRELIMINARY; PRT; 648 AA.
AC 09GY33;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN P2.
GN LM12.121.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC02017.2; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF00560; LRR; 8.
DR PRINTS; PR01217; PRICHEXTENSN.
DR SMART; SM00181; EGF_1.
SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match
Best Local Similarity 8.3%; Score 102.5; DB 5; Length 648;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

OY 4 LAPAWSPTTYLLILLSSGISTGQDSFOHSPISDFAVKIRELSYLLQDYPTVNASN 63
Db 149 LPPWSSMNPINQTLQVRLKLSGT-----LPADMS-SLKSLSNVLEDMPT----- 194
OY 64 LQDEELCGGLMRVLAQRMMERLKTAVAGSKMGGLEERVNEIHVTCARQPP-----S 118
Db 195 -----GL-----LPPBW-----GSLERIQQLVLRKLTGTPLPQWSPMK 229
OY 119 CLAREVO---TWISRLQ-----ETSEQLVALKP-WITRONFSRCLELQCP 160
Db 230 ALRRLTLDTGTLSTGLPQWMSAMASVISLNLEGTVEGTLPPKMSMSRL-QTLNLRRTK 288
OY 161 DSSLTPPPWSPR-----PLEATAPAPQPP-----LILLILPVGLL--LLAAAV 203
Db 289 VSGTLPPWSSMGLANLQSLTGVSTLPQWSSMKRLTQLLTLDTLLSGTLPAEW 345

RESULT 9
OY 09N753 PRELIMINARY; PRT; 345 AA.
AC 09N753;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN P2.
```

```
GN LM12.08.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC02017.2; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 3.
DR SMART; SM00370; LRR; 3.
SQ SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;

Query Match
Best Local Similarity 7.9%; Score 98.5; DB 5; Length 345;
Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;

OY 6 PAMSPPTTYLLILLSSGISTG-----QDCSFOHSPISDFAVKIRELS 49
Db 152 PEMGSMTSLSVLNKGTGISTGLPQWSSGMSKARSLOLQDCLSGSLPSWSAI----- 205
OY 50 DYLLQDYPTVNASNLQDEELCG-----GLMRVLAQRMMERLKTAVAGSKMGGLEERVNTE 104
Db 206 -----PMLASVSLKGNKFCGVCCTRGIRRLVLL--WTSRSTRAATA----- 245
OY 105 IHFVTKCARQPP---PPSCLEFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCP 161
Db 246 --WLRTAQRPPLSPPPRQRPRTSLT-----FPLRRGPR 278
OY 162 SSTLPWSPRRLHATAPAPQPLILL---LLPVGLLLAAACLMQRTTR 212
Db 279 LSRLPQPLRLHRLN-----PPPLRLHRLNPPPLP-----QOTRR 313

RESULT 10
OY 09DWH8 PRELIMINARY; PRT; 1240 AA.
AC 09DWH8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PR2.
GN R2.
OS Rat cytomegalovirus (strain Mastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RC MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RC MEDLINE=20473137; PubMed=11018281;
RA Gruljhujsen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript";
RL Virus Res. 69:119-130(2000).
DR EMBL; AF232689; AAF99111.1; -.
SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match
Best Local Similarity 7.7%; Score 95.5; DB 12; Length 1240;
Matches 33; Conservative 12; Mismatches 57; Indels 101; Gaps 10;
```

Matches	29;	Conservative	8;	Mismatches	18;	Indels	33;	Gaps	5;
QY	160	PDSSTL-----	PPMSPR-DEATAPAPQ-PLLLLLPVGLLLAA	201					
Db	1060	PDSSTAVNGEATERTSTPATERPRPLPGVDSLPLAPQITLLSLTLVRA-----	1112						
QY	202	AWCLHWQRTRRTPRPGQVPPVSPQD	229						
Db	1113	-----QATRASPRPETDAP-PPAD	1132						
RESULT	11								
Q9C5T0		PRELIMINARY;	PRT;	658	AA.				
AC	Q9C5T0;								
DT	01-JUN-2001	(TREMBLrel. 17, Created)							
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)							
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)							
DE	RECEPTOR-LIKE PROTEIN KINASE 4.								
GN	RLK4								
OS	Arabidopsis thaliana (Mouse-ear cress).								
OC	Euxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;								
CC	eutoids II; Brassicales; Brassicaceae; Arabidopsis.								
OX	NCBI_TaxID=3702;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=20575726; PubMed=11135117;								
RA	Du L., Chen Z.;								
RT	"Identification of genes encoding receptor-like protein kinases as								
RT	possible targets of pathogen- and salicylic acid-induced WRKY DNA-								
RT	binding proteins in Arabidopsis."								
RL	Plant J. 24:837-847(2000).								
DR	EMBL; AF244705; AAK28315.1; -								
DR	InterPro: IPR002902; DUF26.								
DR	InterPro: IPR000719; Euk_pkinase.								
DR	InterPro: IPR002290; Ser-thr_pkinase.								
DR	InterPro: IPR001245; Tyr_pkinase.								
DR	Pfam: PF01657; DUF26; 2.								
DR	Pfam: PF00069; pkinase; 1.								
DR	SMART: SMO0220; S_TKc; 1.								
DR	SMART: SMO0219; TyrKc; 1.								
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.								
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.								
KW	ATP-binding; Kinase; Transferase.								
SEQ	SEQUENCE 658 AA; 7291 MW; DCF9C5F1748F614 CRC64;								
Query Match		7.5%;	Score 93.5;	DB 10;	Length 658;				
Best Local Similarity		25.8%;	Pred. No. 0.72;						
Matches	34;	Conservative	16;	Mismatches	39;	Indels	43;	Gaps	6;
QY	138	LYALKPMTIRKQFNSCLL---QCQPD-----	STLPPWMSR	172					
Db	195	LVQCPEDTLRODCSRCLQVINOIPTDRIGARINPSCTSRYEIYAFYTESAVPP--	BP	252					
QY	173	PLEATAPAPAPOP-----	LLLTLLP--VGLLLAAACLHWQRTRRTPP--	217					
Db	253	PSISIPFPAPPRSRKESGSKVLAIVAVPLIIVAVRLFIAIGICFLTRAKRSYSIPSAF	312						
QY	218	-GEQVPPVPSQ 228							
Db	313	AGDDITTDADSLQ 324							
RESULT	12								
ID	017889	PRELIMINARY;	PRT;	1217	AA.				
AC	017889;								
DT	01-JAN-1998	(TREMBLrel. 05, Created)							
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)							
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)							
DE	F54F12.1	PROTEIN.							

GN F54F12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RZ [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z81548; CAB04464.1; -.
DR HSSP: P18052; TYRO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_prot_phptase.
DR Pfam: PF00102; Y_phosphatase; 1.
DR SMART: SM00194; PRPC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
SO Hydroxylase.
SQ SEQUENCE 1217 AA; 135500 MW; 1D1656F460E38508 CRC64;

```

Query Match          7.5%; Score 93; DB 5; Length 1217;
Best Local Similarity 23.6%; Pred. No. 1.7;
Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERKTVAGSGRMQGL---LERNVTEIHFYTKCAQFPSCSLRFQYQINISRLLOETSEQLV 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 627 MDAKAVADGKTSYSVIDALEKLISTMDLDQKCFKFEAPATIKAMDL----FFASVASNIA 682
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 140 ALKRWITRQNFSCNLELQCPDSSLT---PPWSPRLPLATAPAP-----QPIRLILLLL 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 683 ALRQPTTSPTAAAPPIPIPNNGSINGNPSFSSPPLLPVYASSIPATPESNMILYIT 742
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 LPVGLILLAA-----AMCLHWOTRRRRTRRPEQOYPPVSP 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 743 GAVGGLLVYALIGVLEFVFEQKKKKEDKPPD--PPAPLP 781
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
O9GYAL PRELIMINARY; PRT; 560 AA.
AC O9GYAL;
ID 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.
GN LM12.14.
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
   Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AL390114; CAC01954.2; -.
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 13.
DR PROSITE, PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_4.
SQ SEQUENCE 560 AA; 60447 MW; C3ACF96BI059765F CRC64;

```

Best Local Similarity 24.8%; Pred. No. 0.75;
Matches 55; Conservative 27; Mismatches 75; Indels 65; Gaps 11;

OY 4 LAPANSPPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSVDYLLQDPYTVASN 63
DB 124 LPDWSQGLGLSVTLSCGVSQT-----LPASWGLMVRRLRELT----- 162
OY 64 LOD-EELCGGL-----W-----RVLAQRWMEBLKTVAGSKMOGLLEVENTEIHFTVKA 112
DB 163 VADCRHLTGSLPSLMSWLPNLOKLVROLQSLGTLPAWSKVTSLLE---LEIVAAGDIT 219
OY 113 FQPPP--SCLRFVQT-----NISRLQETSEQLVALKP--WITRON 149
DB 220 GTLPPEWSSIKSLRTLNLEGTQVSGTLPPGSEMSKSLTNLELGTQVSGSLPPQWVSMAS 279
OY 150 FSRCLCQCPDSSSTLPPWSPR-----PLEATAPTPAPPP 185
DB 280 L-RTLNLEGTQVSGTLPPGSEMSKSLTNLELGTQVSGTLPP 320

RESULT 14

O9HAD2 PRELIMINARY; PRT; 251 AA.

AC O9HAD2: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, last annotation update)
DE HYPOTHEICAL 26.6 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-EMBRIO;
RA Issigai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nebekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuh Y., Oshima A.;
RA "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK021860; BAB13917.1; -
DR InterPro; IPR002965; P-rich_extensn.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 251 AA; 26607 MW; 420195B27966FD41 CRC64;

Query Match 7.4%; Score 92; DB 4; Length 251;
Best Local Similarity 31.9%; Pred. No. 0.33;
Matches 44; Conservative 9; Mismatches 39; Indels 46; Gaps 10;

OY 115 PPSCLRFVQTNIS-----RLQETSEQLVALKPWITRONFSRCLCQCPDSSSTLPPW 169
DB 76 PPSCLRFVQTNIS-----ALAPQGHPEFSS--RWFHPRITQAPPPG 127
OY 170 SPRPL-ENTAP-----TADQPLLLLLLPVGLLLAAWCLHWQTRRRPRPG 218
DB 128 PPRPLPALVPPQDPHPSPTTQAPPL-----W-LHPRIT--QTPPPG 169
OY 219 EQVPPVSPQDLL-LVEN 235
DB 170 ---PPRPLPALVADPH 184

RESULT 15

O9GYAO PRELIMINARY; PRT; 536 AA.

AC O9GYAO: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.

GN LM12.16.
OS Leishmania major.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC01955.2; -
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 22.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBER; UNKNOWN_7.
SQ SEQUENCE 536 AA; 58020 MW; 41E16B64F667340 CRC64;

Query Match 7.3%; Score 90.5; DB 5; Length 536;
Best Local Similarity 27.2%; Pred. No. 1.1;
Matches 55; Conservative 23; Mismatches 75; Indels 49; Gaps 11;

OY 4 LAPANSPPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSVDYLLQDPYTVASN 63
DB 124 LPDWSQGLGLSVTLSCGVSQT-----LPASWGLMVRRLRELT----- 162
OY 64 LOD-EELCGGL-----W-----RVLAQRWMEBLKTVAGSKMOGLLEVENTEIHFTVKA 112
DB 163 VADCRHLTGSLPSLMSWLPNLOKLVROLQSLGTLPAWSKVTSLLE---LEIVAAGDIT 219
OY 113 FQPPP--SCLRFVQTNISRLQETSEQLVALKP--WITRONFSRCLCQCPDSSSTLPPW 169
DB 220 GTLPPEWSSIKSLRT-----LNLEGTQVSGTLPPGSEMSKSLTN-LELGTQVSGTLPPGW 274
OY 170 S-----PPLEATAPTPAPPP 185
DB 275 SSIKSLRTLNLEGTQVSGSLPP 296

RESULT 16

O9GY15 PRELIMINARY; PRT; 660 AA.

AC O9GY15: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.
GN LM12.151.
OS Leishmania major.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC02034.2; -
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 22.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBER; UNKNOWN_7.
SQ SEQUENCE 660 AA; 71216 MW; E213F39BF1A57BD CRC64;

Query Match 7.3%; Score 90.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.5;
Matches 55; Conservative 23; Mismatches 75; Indels 49; Gaps 11;

OY 4 LAPANSPPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSVDYLLQDPYTVASN 63
DB 8 LPDWSQGLGLSVTLSCGVSQT-----LPASWGLMVRRLRELT----- 46


```

QY 64 LOD-EELCGGL-----W-----RLVLAORMMERLKTVAAGSKMOGLERVTETIHFVTKCA 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 VRDCRHITGSLPISLWMLPNLQKLVRLQLOLSTLPAEMRSVLSLE---LETVAGDITP 103

QY 113 FQPPP--SCLEFVOTNISRLLOETSEQLVALKP-WITRONFSRCLLOCPDSSSTLPPW 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 104 GTLPPEWSSIKSLRT-----LNLBGTQVSGTLPPGWSMKSLTN-LELEGTQVSGTILPPGW 158

QY 170 S-----PRELEATAPPAPOP 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 SSIKSLRTLNLEGTQVSGSLPP 180

```

```

RESULT 17
Q9P36 PRELIMINARY; PRT; 5120 AA.
AC Q9P36;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE ACZONIN (FRAGMENT).
GN ACZ.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99439764; PubMed=10508862;
RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RT Killmann M.W.
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin."
RT J. Cell Biol. 147:151-162(1999).
RL EMBL: Y19187; CAB60725.1; -.
DR HSSP: P04410; 1A25.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR002965; P_rich_extensn.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00595; PDZ; 1.
DR PRINTS: PRO0360; C2DOMAIN.
DR PRINTS: PRO1217; PRICEXTENSN.
DR PRINTS: PRO0399; SYNAPTOTAGMN.
DR SMART: SM00239; C2; 2.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE: PS50004; C2_DOMAIN_2; 2.
DR PROSITE: PS50106; PDZ; 1.
FT NON_TER 1
SQ SEQUENCE 5120 AA; 560751 MW; A658D9891B65B412 CRC64;

```

```

Query Match 7.3%; Score 90.5; DB 13; Length 5120;
Best Local Similarity 24.3%; Pred. No. 17;
Matches 45; Conservative 19; Mismatches 72; Indels 49; Gaps 7;

QY 90 AGSKMOGLERVTETIHF-----VTKAFQPPPSCLRFVQTN----- 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2224 AAKKMSYVETGIKIHEDSHKELSLDMRTNLGTATSEQPLCVASVKEPASETPA 2283

QY 127 --ISRLLOETSE-QLVALKPWITRONF-----SRCLLOCPDSSSTLPPWSPRPLEATAP 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2284 VPTPRVSKSTYSMPSSAPALSKVFSLEFRSSLSLSPAPQSPSPSPPPPPPPPPPPPP 2343

QY 180 TADQP-----PLILLIPVGLLLAAACLIH-WQTRRRTPRPGEGV 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2344 ILPKPAIYPRKKSQIOAPMATAPTAVPLVTSATLESAAVLKNHVVPRVKTTPP-PRV 2402

```

```

QY 222 PPVPS 226
   ||| |||
Db 2403 PPVPS 2407

```

```

RESULT 18
Q17610 PRELIMINARY; PRT; 474 AA.
AC Q17610;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE C28D4.2 PROTEIN.
GN C28D4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
RL EMBL: Z82259; CAB05129.1; -.
DR InterPro: IPR002573; Choline_kinase.
DR Pfam: PF01633; Choline_kinase; 1.
SQ SEQUENCE 474 AA; 54628 MW; DD11C97A1542FEC CRC64;

```

```

Query Match 7.2%; Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%; Pred. No. 1.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TODC-----SFQHS-PISSDPAVKIREL-SDYLLQDYFVTVAASNLQDELQGLMRL 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 TIDCVDLKKVFSKFDSSAPISGEILFRAPFLCAKYL-----GGAMRK 106

QY 77 VLAQRMERLKTVAAGSKMOGLERVTETIHFVTKCAFPDPPSCIR-FVQTNISRLDET- 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 107 VKIEEF--RIRAITGG-MSNLIETVELPAH-LTPIQMEPEKALLRVHCQSDIDLLSESV 162

QY 135 -----SEQLVALKPWITRONFSRCLLOCPDSSSTLPPWSPR--PLEATA 178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 VFTLLSERNLGPKMIGVPPGGREFQIFSRALQCLEISKPELSKLIADIVARVHTLDAP 222

QY 179 PTAPOPPLILLIPVGLLLAAACLIH-WQTRRRTP--RPGE-----QVPPVPSPOD 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 PKEPQ-----TLQTAQQLERF-----KTPAGEPRIMLYLQAQVPPKSDVPST 266

QY 230 LLIVE 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 ITVAQ 271

```

```

RESULT 19
Q9QMT1 PRELIMINARY; PRT; 270 AA.
AC Q9QMT1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NK744R62 PROTEIN.
GN NK744R62.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

```

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=LYMPHOID;
 RC Cantoni C., Blassoni R.;
 RT "Mkp4 related genes";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ010100; CAB52290.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IG_1.
 SQ SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;
 Best Local Similarity 23.0%; Pred. No. 0.8; 112; Indels 77; Gaps 15;
 Matches 63; Conservative 22; Mismatches 77; Gaps 15;

QY 7 AMSPTVYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLDYPTVYASNLQD 66
 DB 2 AMRALHPLLLLLLFPGSQASKAQLVQSVAGQTLVRCQ-----YPT----- 45
 QY 67 EELGGIM-----RLVLAQR-----MMERLKYAGSKMOGLERVTET- 105
 DB 46 ---GSLYEKKGCKEASALVCLRLVTSKPRITWMTSRF-TIWDPDAGFTVTMTDLR 100
 QY 106 ----HFVTKCAFQPPPSCLRFVQNTISRLQETSEQLVALKWPITRONFSRCLEIQ-CQ 159
 DB 101 EEDSGH--WCRIYRPD--NSVSKSVRYLIVSPASASQOTWTPRDVLSQOTQSCV 156
 QY 160 PDS-----STLPPWSP-RPLDAPAPAPQ-----PILLLLLPV--GLI--- 197
 DB 157 PPTAGARQAPESPSTIIVPSHSPSLPVPPLPSRQNSTLRRPAPALVAVPCGLIVAK 216
 QY 198 -LLAAMCIHQWQRRRTPRREGV--PVPSQ 228
 DB 217 SLVSLIIVWVYLRNRMHQGRSLHPAOPRPQ 250

RESULT 20
 Q9AMJ4
 ID Q9AMJ4 PRELIMINARY; PRT; 404 AA.
 AC Q9AMJ4;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE P0489A05.3 PROTEIN.
 GN P0489A05.3
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0489A05.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003105; BAB32983.1; -
 DR InterPro: IPR000480; Glutelin.
 DR PRINTS; PR00211; GLUTELIN.
 SQ SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;
 Best Local Similarity 26.1%; Pred. No. 1.3; 88; Indels 75; Gaps 17;
 Matches 66; Conservative 24; Mismatches 88; Indels 75; Gaps 17;

QY 4.33 QHSPISDF-AVKIRESDYLDYPTVYASNL-----QDEELCGGLMRLV 78
 DB 107 RHSELSFSELEKVOITPLKTVWSMNPPLKPKNOFTFLINRYQKNSPEOLCKRFW---- 162

QY 79 AQRMMERLKTIVAGSKMOG---LLERVNT--ELHFVTKCAFQPPPSCLRFVQNTI---SRL 130
 DB 163 -STWOSNAGAT-GSRAGSERLIRPPSSAGRRPMLVPPSPPPASLAAQVFNALTSRA 220
 QY 131 LQETSEQLVALKWPITRONFSR---CLEIQ--COPDSSTLP-----PPWSRPLEAT 177
 DB 221 LSATG-----TPTTSSILRRPLHCLLPRLAPRPPSILPLPLQAPPHPPLP---P 271
 QY 178 APTAQPPLLLLLL-----PV-----GLL-----LLAAMCIHQWQRRRTPR 216
 DB 272 PPTARAPPLAVCLRLCPILPKPPVAGGLFVAHSAITAVLQAGCV--RLHRRPLR 329
 QY 217 P--GEQVPPVPS 227
 DB 330 PPSSLLPLSRAP 342

RESULT 21
 Q943D5
 ID Q943D5 PRELIMINARY; PRT; 1267 AA.
 AC Q943D5;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PUTATIVE RECEPTOR SERINE/THREONINE KINASE.
 GN P0443D08.17.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0443D08.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003250; BAB4138.1; -
 KW Receptor; Kinase.
 SQ SEQUENCE 1267 AA; 136583 MW; 062P0C27C5490D75 CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 1267;
 Best Local Similarity 22.0%; Pred. No. 5; 96; Indels 71; Gaps 11;
 Matches 54; Conservative 24; Mismatches 96; Indels 71; Gaps 11;

QY 22 SGLSGTDCSFQHS-----PISSDFAVKIRELSDYLDYPTVYASNLQDEELCGGLMRLV 77
 DB 725 AREGTAPCDLRLRGIVVVVADPAAARARKTEAGTQ---TEGGRWSSPACGGRAAAS 780
 QY 78 LAQRMMERLKTIVAGSKMOGLERVNTIELHFVTKCAFQPPPSCLRFVQNTISRLQETSEQ 137
 DB 781 RARR-----KEBAGARGVYTAARRSSP-----ARKGEAPPPDLRLI-----YPAAGS 824
 QY 138 LVALKWPITRONFSRCLEIQCPDSSTLPWPWSPRPLEATAPTA----- 181
 DB 825 TACTPWPPELHHN-----RCSSSSSSSPSP--PRLGATAPTAARCSHKSAPPRAPSD 876
 QY 182 -----PQPLLLLLLP-----VGLLLLAAMCIH--WQRRRTPRREGVPPVP 225
 DB 877 RRRRLSSPPPPQIVAAASDRRLGPPQIAAAALHHNEWALA-----GQCLTPPP 929
 QY 226 SPQDL 230
 DB 930 PPPQL 934

RESULT 22
 ID 075064 PRELIMINARY; PRT; 1386 AA.
 AC 075064;
 ID 075064;
 AC 075064;

DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIA0476 PROTEIN.
 GN KIA0476.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=98116662; PubMed=9455484;
 RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
 Nomura N., Ohara O.;
 RT "Characterization of cDNA clones in size-fractionated cDNA libraries
 from human brain";
 RL DNA Res. 4:345-349(1997).
 DR EMBL; AB007945; BAA32321.1; -.
 DR InterPro; IPR001194; DENN.
 DR InterPro; IPR002885; PPR.
 DR Pfam; PF02141; DENN; 1.
 DR Pfam; PF01535; PPR; 1.
 DR SEQUENCE 1386 AA; 15229 MW; BE960E7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;
 Best Local Similarity 23.1%; Pred. No. 5.6;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;
 QY 21 SSGLSSTOCPSFOHSPISDFVAKRELSDVILQDYPTVANSNLODELCL---GGLRL 76
 DB 1104 SAGASSSKDAPYVGGP-----GVLSDRRCLLA--LDEPOLCGHMGASRR 1148
 QY 77 VLAQRMERLKTVAASKMOGLERVTETHEVTKCAFQPPSCRFVQTNISRLLOETSE 136
 DB 1149 VESGAWAYLSPVLKRELESTIVENEGSEV-----LALPELSAHLIFIMNLWYFQRL- 1201
 QY 137 QLVAKPMITRQNFRCLELQCO-PDSSLTLPWP-SPRPLA-----TATPAQPP 185
 DB 1202 RLPSILIPGLVLAAS-----CDGFSHSDAPSPWLTLPSPASVOYRLMDVLTLPSPNSCP 1253
 QY 186 LLLLLLPVGLLLAAWCLHMORTRRTPRPGEOVPVPSPDILLVE 234
 DB 1254 LVYL-----WRVHSQ-IPQRYVMG---PVPAISLALLE 1284

RESULT 23
 ID Q9GKE2 PRELIMINARY; PRT; 250 AA.
 AC Q9GKE2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SR-PSOX.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20576214; PubMed=11060282;
 RA Shinaka T., Kume N., Minami M., Hayashida K., Kataoka H., Kita T.,
 Yonehara S.;
 RT "Molecular Cloning of a Novel Scavenger Receptor for Oxidized Low
 Density Lipoprotein, SR-PSOX, on Macrophages";
 RL J. Biol. Chem. 275:40663-40666(2000).
 DR EMBL; AF277000; AAG31753.1; -.
 DR SEQUENCE 250 AA; 27569 MW; 6A4DCFA55C35421E CRC64;

Query Match 7.1%; Score 88; DB 6; Length 250;
 Best Local Similarity 24.2%; Pred. No. 0.82;

Matches 64; Conservative 33; Mismatches 100; Indels 68; Gaps 14;
 QY 6 PMSPTYLLILLIL-----SSGLSGTQDCS---FOHSPISDFAVKIKELSDYL- 52
 DB 2 PMSPTYLLILLILFLAFLMLPPGNGNEGSMAGSCPNNRISHSPTDH--DMRLRLRYLN 58
 QY 53 -LQDPVTVASVLODEELCGGLMLRLVLAQRMERL-----KTVGSKMOGL 97
 DB 59 HYQCTSYVRQLPRGSCGG-----SSDQVYKLKMGCFDRGEGRAHATVA---HQCH 110
 QY 98 LERVNTEIHEVTKCAFQPPSCLEFVQTNISRLLOETSEOLVALKPWTR--ONFSRCLE 155
 DB 111 LAPONTTRVPELPERA---PPDSTPAQTNPSTQPTQ-----KPLPEGMPSLAKKIL 161
 QY 156 LQCPDSSLTLPWPSPRP-----LEATPAQPP--LILLLLPVGILLLA 200
 DB 162 PISENDISTVGSLSLCAKSEARENDEQLCKNGATGTSALVPVLSLYIFLLTGVLTY- 220
 QY 201 AAWCLHMORTRRTPRPGEOVPVP 225
 DB 221 -VMCKKROGSHQYP-PDPQLHYVP 243

RESULT 24
 ID Q9DBT2 PRELIMINARY; PRT; 675 AA.
 AC Q9DBT2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 1200014H2ARIK PROTEIN.
 GN 1200014H2ARIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
 Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner U., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsaki S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AK004763; BAB23544.1; -.
 DR HSSP; Q15843; 1IND
 DR MGD; MGI:1914715; 1200014H2ARIK.
 DR InterPro; IPR002965; P_rich_extensn.
 DR InterPro; IPR000061; Surp.
 DR InterPro; IPR000626; Ubiqultin.
 DR Pfam; PF01805; Surp; 1.
 DR Pfam; PF00240; Ubiqultin; 1.
 DR PRINTS; PR01217; PRICHEXTNSN.
 DR SMART; SM00213; UBO; 1.
 DR PROSITE; PS50053; UBIQUITIN_2; 1
 DR SEQUENCE 675 AA; 75703 MW; 3039679A63FED85EF CRC64;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:34:09 ; Search time 53.63 Seconds

(without alignments)
486,712 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MTVLAPAPMSPTYLILLLL.....RPGQVPVPSPQDLLVEH 235

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum first 50 summaries

Database :
1: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SID55/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID55/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand
2	1242	100.0	235	20	AA67769 Human flt3-ligand
3	1242	100.0	235	21	AAV69719 Full length wild t
4	1242	100.0	235	22	AA620192 Human flt-3 ligand
5	1236	99.5	235	16	AA66175 Human S86/S109 flt
6	1236	99.5	235	22	AA620194 Human flt-3 ligand
7	1124	89.7	209	19	AA69721 Human flt-3 mutain
8	1114	89.7	209	19	AA69007 Human flt-3 recept
9	1114	89.4	209	21	AAV69720 Mature wild type h
10	1110	89.4	209	21	AAV69723 Human flt-3 mutain
11	1110	89.4	209	21	AAV69726 Human flt-3 mutain

12	1110	89.4	209	21	AAV69727 Human flt-3 mutain
13	1110	89.4	209	21	AAV69729 Human flt-3 mutain
14	1108	89.2	209	21	AAV69722 Human flt-3 mutain
15	1108	89.2	209	21	AAV69724 Human flt-3 mutain
16	1107	89.1	209	21	AAV69728 Human flt-3 mutain
17	1100	88.6	209	21	AAV69725 Human flt-3 mutain
18	970	78.1	294	21	AA620195 Human flt-3 ligand
19	895.5	72.1	294	21	AAV58204 Canine flt-3 ligand
20	894.5	72.0	191	21	AAV58210 Canine flt-3 ligand
21	834	67.1	178	22	AA620193 Human flt-3 ligand
22	797.5	64.2	268	21	AAV58206 Canine mature flt-
23	796.5	64.1	276	21	AAV58207 Canine flt-3 ligand
24	791.5	63.7	265	21	AAV58211 Canine mature flt-
25	768.5	61.9	231	16	AA67540 Mouse mature flt-
26	768.5	61.9	231	20	AA67768 Murine flt3-ligand
27	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
28	768	61.8	232	12	AA66177 Mouse MOR110/T118
29	764	61.5	232	22	AA620189 Mouse flt-3 ligand
30	745	60.0	150	19	AAW77930 Flt3 ligand FL110C
31	745	60.0	150	19	AA669054 Human flt-3 recept
32	740.5	59.6	377	19	AAW78124 Chimeric receptor
33	739	59.5	143	19	AAW77926 Flt3 ligand FL13C.
34	739	59.5	143	19	AAW69050 Human flt-3 recept
35	737.5	59.4	349	19	AAW83289 Human flt3 ligand
36	737.5	59.4	349	19	AAW8005 Human flt3 ligand
37	736.5	59.3	340	19	AAW83291 Human flt3 ligand
38	736.5	59.3	349	19	AAW83286 Human flt3 ligand
39	736.5	59.3	523	19	AAW78008 Trimeric flt3L-G-C
40	735	59.2	140	19	AAW77911 Human flt3 ligand
41	735	59.2	140	19	AAW69035 Flt3 ligand FL14C.
42	735	59.2	144	19	AAW77928 Human flt-3 recept
43	735	59.2	144	19	AAW69052 Human flt-3 recept
44	735	59.2	313	19	AAW83294 Human flt3 ligand
45	733.5	59.1	286	19	AAW83303 Human flt3 ligand
46	733.5	59.1	286	19	AAW7952 Human flt-3 and IL-3 chl
47	733.5	59.1	314	19	AAW83293 Human flt3 ligand
48	733.5	59.1	314	19	AAW8004 Dimeric flt3 ligand
49	733.5	59.1	460	19	AAW78007 Trimeric flt-3 rece
50	733.5	59.1	523	19	AAW78006 Trimeric flt3L-G-C

ALIGNMENTS

RESULT 1	
ID	AA67541 standard; Protein; 235 AA.
XX	
AC	AA67541;
XX	
DT	05-AUG-1995 (first entry)
XX	
DE	Human flt-3 ligand.
XX	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	1..26
FT	/label= sig_peptide
FT	/note= "signal peptide may extend to position 27"
FT	27..182
FT	/label= Extracellular_domain
FT	/note= "extracellular domain may start at position 28"
FT	183..205
FT	/label= Transmembrane_domain
FT	206..235
FT	/label= Cytoplasmic_domain
XX	
PN	EP627487-A.
XX	

XX	12-JUN-1998:	98WC-US12085.
PE		
PR	17-JUN-1997:	97US-0877421.
XX		
XX	(IMMUNEX) IMMUNEX CORP.	
PA		
XX		
PI	Abbott NM, Mowat AM, Viney JL;	
XX		
DR	WPI; 1999-070422/06.	
DR	N-PDB; AAV81506.	
PT		
PT	Methods for initiating or enhancing antigen specific immune	
XX	tolerance - By using murine or human flt3 ligand	
XX		
XX	Claim 1; Page 14-15; 25pp; English.	
XX		
CC	A method has been developed of initiating or enhancing: (i) an antigen-	
CC	specific immune tolerance; or (ii) immunotolerance of a therapeutic	
CC	immunogenic molecule by addition of a polypeptide, before, after or with	
CC	the mucosal administration of an immunotolerising amount of the antigen	
CC	or therapeutic molecule, respectively. The polypeptide is capable of	
CC	binding the flt3 receptor and is: a) amino acids 28-x of murine flt3	
CC	ligand (flt3-L), where x is an amino acid between 163-231; b) amino	
CC	acids 28-y of human flt3-L, where y is an amino acid between 160-235;	
CC	and c) a polypeptide that has at least 90% identity to the polypeptides	
CC	of either (a) or (b). The method ameliorates the effects of autoimmune	
CC	diseases, food allergies or organ or tissue rejection following	
CC	transplantation. Administration of flt3-L allows lower doses of antigens	
CC	to be used in vivo for mucosally administered antigens. The present	
CC	sequence represents human flt3-L.	

	Query Match	100.0%;	Score 1242;	DB 20;	Length 235;
	Best Local Similarity	100.0%;	Pred. No. 4.1e-109;		
	Matches 235; Conservative	0;	Mismatches	0;	Gaps
QY	1 MTVALPAPMSPTTLLILLLLSSGSGISGNODCSFQHSPPSSDFAVKIRELSPLYLLQDPVPTY 60				
Db	1 mtylapawspcty111111ssglsqgdcsfqhspsisdfavkirelsdylllqdpvrv 60				
QY	61 ASNLODELGGIMRLVLQAQRMMERLKTVAAGSKMOGLLEKRVNTEIFHYTKCAFPQPSCSL 120				
Db	61 asnlqdeeleqglwrlvlaqgrmerlkttvasgmkgllervnteihfvtckafqppscsl 120				
QY	121 RFVQTNRSLLOETSEQVALAKPWITRQNRSRLGLEQCOPDSSLTLPMPMSRRLEATAPT 180				
Db	121 rfvgtnsrillgetseqvalakpwitrgnfrsclelqcqpdssltlpmpwsrprrleatapt 180				
QY	181 APQEPFLLLLPLPGGLLLAAACCLHMQRFRRRPRRGEOVPVPSPQDLLVEH 235				
Db	181 apqppl111111pyg1111laaacclhwqrtrrrrtprpgqvvpvppqd111veh 235				
RESULT	3				
ID	AAV69719				
XX	AAV69719 standard; Protein; 235 AA.				
AC	AAV69719;				
XX					
DT	05-JUL-2000 (first entry)				
XX					
DE	Full length wild type human flt-3 protein.				
KW	Immunomodulator; immunosuppressive; cytosstatic; anti-anemic; anti-HIV;				
KM	neuroprotective; antiallergic; FLT3 ligand; FLT3-L; wild type; allergy;				
KM	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;				
KM	cellular expansion; cellular differentiation; natural killer cell;				
KM	cancer; dendritic cell; immune response; autoimmunity; immunosuppression				
KM	myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;				
XX	multiple myeloma; leukemia.				
XX					

OS Homo sapiens.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99MO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMUNEX) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX WPI: 2000-182115/16.
DR N-PSDB; AAZ59064.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
PS Claim 1; Page 72-73; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (this sequence) or mature (AA69720) flt3-L
CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
CC receptors and regulate growth and differentiation of hematopoietic
CC progenitor cells. The flt3-L protein can be used to induce cellular
CC expansion (especially in vivo) or differentiation, e.g. in
CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
CC presence of growth factors such as interleukins, colony stimulating or
CC factors or protein kinases. The protein can also modulate, augment or
CC enhance a patient's immune response and can be used to treat an immune
CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
CC may be used to treat a pathological condition e.g. myelodysplasia,
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
CC leukemia.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 21; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDPAVKIRELSDYLDYPTV 60
DB 1 mtlvapawspptylllllllssgsgtcdcfqhspsissdtafvkirelsdyllldypvtv 60
QY 61 ASNLDEELCGGLMRVLVAORMERLKTVAAGSKMGGILLERVNTEIHFTVKCAFQPPPSCL 120
DB 61 asnldeelcggllmrvlvaqrmwmerlktvagskmggillervnteihftvkcafqpppscl 120
QY 121 RRVQVNIIRSLDETSQVLAALKPWITRNFRCLELQCOQPSSTIRPPWSRRLPEATAPT 180
DB 121 rrvqvnirsldeetsqvalalkpwittrnfrclelqcqpsstirppwsrprleatapt 180
QY 181 APQPLLILLPLVGLLLAAAMCLHMQRTRRRPRPEEQVPPVPSDDLLVENH 235
DB 181 apqppllllllllpyglllllaaawclhwqrtrrrprpgeqvppvpsddlllvhen 235

XX
KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /Label= Signal_peptide
FT Protein 27..235
FT /Label= Mature_protein
FT Domain 27..182
FT /Label= Extracellular_domain
FT Domain 183..205
FT /Label= Transmembrane_domain
FT Domain 206..235
FT /Label= Cytoplasmic_domain
XX
PN WO2000109303-A2.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000MO-US20679.
XX
PR 30-JUL-1999; 99US-0146170.
XX
PA (VICA-) VICAL INC.
XX
PI Hermanson GG;
XX
DR WPI: 2001-123319/13.
DR N-PSDB; AAF30310.
XX
PS Immunogenic compositions comprising Flt-3 ligand encoding
PS polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 132-133; 149pp; English.
XX
PS The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
CC or 27-235 of the ligand. The polynucleotides are incorporated
CC into the cells of the vertebrate in vivo, and a prophylactically
CC or therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDPAVKIRELSDYLDYPTV 60
|||||

```

Db      1 mtlvapawspptylllllllllssglsqtqdcsfqhsplsdafvakiirelstdyllqdyptv 60
QY      61 ASNIODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTYKCAFQPPPSCL 120
Db      61 asnlqdeelcggllwrlvlaqrwmerlktvagskmgllervnteihftvkaafqpppscl 120
QY      121 RFVQTNISRLQETSSEQLVAKPMTTRQNFRCLELOCQPDSSLTLPWSPRPLEATAPT 180
Db      121 rfvgtnisrllqetseqlvalkpwttrqnfsrclelqcpdssclppwspripeatapt 180
QY      181 APQPLLILLLLPVGILLAAAWCLHMQRTRRRTRPGEQVPVPSPODLLLVEH 235
Db      181 apqpllilllllllpyglllllaawclhwqtrrrtrrpgeqvppvspqdilllveh 235

RESULT 5
AAR6175
ID      AAR6175 standard; Peptide; 235 AA.
XX
AC      AAR6175;
XX
DT      10-AUG-1995 (first entry)
XX
DE      Human S86/S109 Flt3 ligand peptide sequence.
XX
KM      Flt3 ligand; tyrosine kinase receptor ligand.
XX
OS      Homo sapiens.
XX
PN      WO9426891-A.
XX
PD      24-NOV-1994.
XX
PE      18-MAY-1994; 94MO-US05150.
XX
PR      19-MAY-1993; 93US-0065231.
PR      07-JUL-1993; 93US-0089263.
PR      16-JUL-1993; 93US-0092549.
PR      13-AUG-1993; 93US-0106340.
PR      24-AUG-1993; 93US-0112391.
PR      19-NOV-1993; 93US-0155111.
PR      03-DEC-1993; 93US-0162413.
XX
PA      (INRM ) INST NAT SANTE & RECH MEDICALE.
PA      (SCHE ) SCHERING CORP.
XX
PI      Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
XX
DR      WPI; 1995-006787/01.
DR      N-PSDB; AAO79642.
XX
PT      New ligand for the Flt3 tyrosine kinase receptor - and related
PT      nucleic acid, vectors, host cells and antibodies, useful for
PT      treating abnormal cell physiology and proliferation, e.g. cancer,
PT      also for diagnosis and drug screening
XX
PS      Claim 11: Page 76-77; 90pp; English.
XX
XX
XX      A cDNA library from the human stromal cell line 295SV48, in
XX      pHEB5, was screened with an 800 bp fragment derived from
XX      mouse clone T118. This fragment encompasses the coding region
XX      conserved between two mouse clones, T118 and T110. Approx. 20
XX      CC positive clones were selected and partially sequenced. Two
XX      CC clones, S86 and S109, were found to be approx. 75% homologous
XX      CC to the mouse clones over the first 163 AAs. Clone S86 continued
XX      CC to show homology to T110 until the stop codon, although to a
XX      CC lesser degree, for an overall homology of 66%. Clones T118 and
XX      CC S109 do not show homology to each other or to the other clones
XX      CC after mouse residue 163 (human residue 160). An additional mouse
XX      CC clone designated M8 has a 29 AA insert at the junction between
XX      CC the common and divergent portions of the mouse ligand.
XX
XX      Sequence 235 AA:

```

```

Query Match          99.5%; Score 1236; DB 16; Length 235;
Best local similarity 99.6%; Pred No. 1.5e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSPHSPISDSFAVKIIRLSDYLLQDYPYTV 60
Db      1 mtlvapawspptylllllllssglsqtqdcsfqhsplsdafvakiirelstdyllqdyptv 60
QY      61 ASNIODEELCGGLMRLVLAQRMERLKTAVAGSKMGLLERYNTEIHFTYKCAFQPPPSCL 120
Db      61 asnlqdeelcggllwrlvlaqrwmerlktvagskmgllervnteihftvkaafqpppscl 120
QY      121 RFVQTNISRLQETSSEQLVAKPMTTRQNFRCLELOCQPDSSLTLPWSPRPLEATAPT 180
Db      121 rfvgtnisrllqetseqlvalkpwttrqnfsrclelqcpdssclppwspripeatapt 180
QY      181 APQPLLILLLLPVGILLAAAWCLHMQRTRRRTRPGEQVPVPSPODLLLVEH 235
Db      181 apqpllilllllllpyglllllaawclhwqtrrrtrrpgeqvppvspqdilllveh 235

RESULT 6
AAB20194
ID      AAB20194 standard; Protein; 235 AA.
XX
AC      AAB20194;
XX
DT      14-MAY-2001 (first entry)
XX
DE      Human Flt-3 ligand.
XX
KM      Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KM      immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KM      lymphoma; autoimmune disease; infection; gene therapy.
XX
OS      Homo sapiens.
XX
XX
XX      Key      Location/Qualifiers
XX      FH      Peptide      1..26
XX      FT      Protein      /label= Signal_peptide
XX      FT      Domain      /label= Mature_protein
XX      FT      Domain      /label= Extracellular_domain
XX      FT      Domain      /label= Transmembrane_domain
XX      FT      Domain      206..235
XX      FT      Domain      /label= Cytoplasmic_domain
XX
XX      WO200109303-A2.
XX
XX      08-FEB-2001.
XX
XX      31-JUL-2000; 2000WO-US20679.
XX
XX      30-JUL-1999; 99US-0146170.
XX
XX      (VICA-) VICAL INC.
XX
XX      Hermanson GG;
XX
XX      WPI; 2001-123319/13.
XX      N-PSDB; AAF30312.
XX
XX      Immunogenic compositions comprising Flt-3 ligand encoding
XX      PT polynucleotide and one or more antigen, or cytokine encoding
XX      PT polynucleotides, useful for suppressing tumour growth and for treating
XX      PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX      Claim 2; Page 137-138; 149pp; English.

```

CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
CC of the Flt-3 ligand. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

CC
XX
SQ Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 22; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.5e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYTLAPAMSTYTLILLILLSSGLSTGQCSFQHSPISSDFAKIRELSDYLLQDPVTV 60
DB 1 mvtlapawspctyllillissglsgtdcsfqhspsidssdfavkirelsdyllqdpvtt 60
QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
DB 61 asnlqdelelqglwrlvlaqrmerlktvagskmglldernteihfvtkcafpqpscl 120
QY 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLERLQCCPDSTLPPMSPRLEXTAFT 180
DB 121 rfvgtnisrllqetseqvlakfpwitrqnfsrclelqcpdastclppwsprileaft 180
QY 181 APOPELILLLLPVGLLLLAAMCLMORTRRRTPRPGEOVPVPSPODLLVEH 235
DB 181 appeplllllllpvglilllaawclmwqtrrrtrtpgqevppvpqdlllveh 235

RESULT 7

AAV69721
ID AAV69721 standard; Protein; 212 AA.

XX
AC AAV69721;

DT 05-JUL-2000 (first entry)

XX
DE Human flt-3 mutein L-3H.

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; Flt3 ligand; Flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.

XX
OS Homo sapiens.
OS Synthetic.

PN WO200001823-A2.

XX
PD 13-JAN-2000.

XX
PF 25-JUN-1999; 99WO-US14296.

XX
PR 02-JUL-1998; 98US-0109100.

XX
PA (IMMUNEX CORP.

XX
PI Graddis JT, McGrew JT;

XX
DR WPI; 2000-182115/16.

PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
CC immune response stimulation or treatment of pathological conditions
CC contains amino acid substitutions at positions 8, 84, 118 or 122 -
CC Claim 4; Page 79-80; 90pp; English.

PS The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
XX which exhibits increased or decreased biological activity relative to
XX the full length wild type (AAV69719) or mature (AAV69720) flt3-L
XX polypeptides. This sequence represents an example of the novel flt3-
XX ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
XX binds cell surface tyrosine kinase receptors and regulate growth and
XX differentiation of hematopoietic progenitor cells. The flt3-L protein can
XX be used to induce cellular expansion (especially in vivo) or
XX differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
XX cells, especially in the presence of growth factors such as interleukins,
XX colony stimulating factors or protein kinases. The protein can also
XX modulate, augment or enhance a patient's immune response and can be used
XX to treat an immune disorder (e.g. allergy, autoimmunity or
XX immunosuppression). The protein may be used to treat a pathological
XX condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
XX small cell lung, testicular or ovarian cancer, lymphoma, multiple
XX myeloma, neuroblastoma or acute leukemia.

SQ Sequence 212 AA:

Query Match 90.5%; Score 1124; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.9e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SCTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTVASNLQDEELCGGLMRLVLAQRME 84
DB 2 sctqdcsfqhspsidssdfavkirelsdyllqdpvtrvaasnlqdeelcgglwrlvlaqrme 84
QY 85 RKTVAAGSKMGLERVNTIEHFVTKCAFQPPSCLRFVQTNISRLQETSEQLVAKPW 144
DB 62 rktvagskmglldernteihfvtkcafpqpsclrfvqtnisrllqetseqvlakpw 121
QY 145 ITRONFSRCLERLQCCPDSTLPPMSPRLEXTAFTAPOPDLLLLPVGLLLLAAMC 204
DB 122 itrqnfsrclelqcpdastclppwsprileaftapppdllllllpvglilllaawc 181
QY 205 LHMORTRRRTPRPGEOVPVPSPODLLVEH 235
DB 182 lhwqtrrrtrtpgqevppvpqdlllveh 212

RESULT 8

AAV69007
ID AAV69007 standard; peptide; 209 AA.

XX
AC AAV69007;

DT 01-OCT-1998 (first entry)

XX
DE Human flt-3 receptor agonist.

KW Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
KW bone marrow reconstitution; haematological disease; immune deficiency;
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
KW congenital metabolic disease; neurological disease; therapy;
KW dendritic cell production.

OS Homo sapiens.
 XX WO9818923-A1.
 XX 07-MAY-1998.
 XX 23-OCT-1997; 97WO-US18700.
 XX 25-OCT-1996; 96US-0030094.
 XX (SEAR) SEARLE & CO G D.
 XX
 PI Feng Y, McKearn JP, McWhirter CA, Minnerly JC, Munster NI;
 PI Stalen NR, Streeter PR, Wolfe SL;
 XX WPI: 1998-272218/24.
 DR
 XX
 PT Rearranged flt-3 receptor agonists and nucleic acids encoding them -
 PT used to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of haematological diseases, bone marrow reconstitution
 PT and in gene therapy
 PS
 PS Disclosure: Page 9-10; 158bp; English.
 XX
 CC This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or refold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.
 XX
 XX Sequence 209 AA;
 SQ
 Query Match 89.7%; Score 1114; DB 19; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.2e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVASNLQDELCGMLRLVLAQRMERL 86
 DB 1 tqdcstfghpsissdfavkirelsdyllqdyptvasnlqdeecoglwrlvlaqrmerl 60
 QY 87 KTVAGSKMOGLLEVRNTEHFVTKARQPPSCLEFVQTNISRLQETSEDLVALKRWIT 146
 DB 61 ktvagskmqgllervntehtfvtkarqppscrlrfvqtnisrlilqetseqvlalkpwit 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLPLVGLLLAAACILH 206
 DB 121 rqnfsrcllelqcpdssstlppwsprrpleatcapapqpllllllpvgllllaaacilh 180
 QY 207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
 DB 181 wqtrrrtrprgeqvppvpspdllyeh 209
 RESULT 9
 ID AAY69720
 AC AAY69720; standard; Protein; 209 AA.

XX 05-JUL-2000 (first entry)
 DT Mature wild type human flt-3 protein.
 XX
 DE
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; haematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200001823-A2.
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 PF
 XX 02-JUL-1998; 98US-0109100.
 PR
 XX (IMM) IMMUNEX CORP.
 PA
 XX Gradalis TJ, McGrew JT;
 PI
 PI WPI: 2000-182115/16.
 DR N-PSDB: AA259064.
 XX
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 PS
 PS Claim 1: Page 89-90; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 XX
 XX Sequence 209 AA;
 SQ
 Query Match 89.7%; Score 1114; DB 21; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.2e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVASNLQDELCGMLRLVLAQRMERL 86
 DB 1 tqdcstfghpsissdfavkirelsdyllqdyptvasnlqdeecoglwrlvlaqrmerl 60
 QY 87 KTVAGSKMOGLLEVRNTEHFVTKARQPPSCLEFVQTNISRLQETSEDLVALKRWIT 146
 DB 61 ktvagskmqgllervntehtfvtkarqppscrlrfvqtnisrlilqetseqvlalkpwit 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLPLVGLLLAAACILH 206
 DB 121 rqnfsrcllelqcpdssstlppwsprrpleatcapapqpllllllpvgllllaaacilh 180
 QY 207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235

Db 181 wqrrrrrcprgpgvpyppsqdillllehh 209
|||||
RESULT 10
ID AAY69723 standard; Protein: 209 AA.
XX AAY69723;
XX AAY69723;
XX 05-JUL-2000 (first entry)
XX Human flt-3 mutein K84E.
DE
KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;
KW neuroprotective; antiangiogenic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200001823-A2.
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99MO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMUV) IMMUNEX CORP.
XX
PI Gradalis TJ, McGrew JT;
DR WPI: 2000-182115/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
PS
PS Claim 4; Page 84-85; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
CC
SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best local similarity 99.5%; Pred. No. le-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0

27 TQDCRPHSHISSDFAVKTRLSYLDQDPYTVAASNIQDELGGMLRWLAQRMMERL 86
1 tqdcshpsissdfavktrlsdyldqpyvtvasniqdeqlcgmlrwlvlaqrmmrl 60

OY	87	KIVASKNQGLIERNTEIHVTCACAPRPSCLRFQVNTISLLOETSQVLAKPMT	146
Dd	61	kcvasskmqglilervntehfvtccatqpsscrlrtvqnlsrlqlqeseqvalkpwlt	120
OY	147	RONFSRCLELOCQPDSSITLPFPMSPRELEATAPAPQPRLILLPLPGVLLIAAMCIIH	206
Dd	121	rqnfrscrlclqcqpdssitlppwsprrpleastaparppllllllllpvglllllaawcjh	180
OY	207	WQRRTTRTPRGPEOVPPYPSPODLLVEH	235
Dd	181	wqrtrtrprpgpeqvpyppspqdlllvch	209
 RESULT 11 AA69726 ID AAY69726 standard; Protein; 209 AA.			
AC	AA69726;		
DT	05-JUL-2000	(first entry)	
DE	Human flt-3 mutain Q122R.		
XX			
KM	Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;		
KM	neuroprotective; anti-allergic; Flt3 ligand; Flt3-L; wild type; allergy;		
KM	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;		
KM	cellular expansion; cellular differentiation; natural killer cell;		
KM	cancer; dendritic cell; immune response; autoimmunity; immunosuppression;		
KM	myeloid plasma; aplastic anemia; HIV infection; lymphoma; neuroblastoma;		
XX	multiple myeloma; leukemia; mutain.		
OS	Homo sapiens.		
OS	Synthetic.		
PN	WO200001823-A2.		
PD	13-JAN-2000.		
XX			
PF	25-JUN-1999;	99MO-US14296.	
XX			
PR	02-JUL-1998;	980S-0109100.	
XX			
PA	(IMMV) IMMUNE CORP.		
PI	Graddis TJ, McGrew JT;		
DR	WPI: 2000-182115/16.		
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,		
PT	immune response stimulation or treatment of pathological conditions		
XX	contains amino acid substitutions at positions 8, 84, 118 or 122 -		
PS	Claim 4; Page 88-89; 90pp; English.		
XX			
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides		
CC	which exhibits increased or decreased biological activity relative to		
CC	the full length wild type (AAY69719) or mature (AAY69720) flt3-L		
CC	polypeptides. This sequence represents an example of the novel flt-3		
CC	ligands and comprises the Q122R mutant polypeptide. The flt3-L protein		
CC	binds cell surface tyrosine kinase receptors and regulate growth and		
CC	differentiation of hematopoietic progenitor cells. The flt3-L protein can		
CC	be used to induce cellular expansion (especially in vivo) or		
CC	differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic		
CC	cells, especially in the presence of growth factors such as interleukins,		
CC	colony stimulating factors or protein kinases. The protein can also		
CC	modulate, augment or enhance a patient's immune response and can be used		
CC	to treat an immune disorder (e.g. allergy, autoimmunity or		
CC	immunosuppression). The protein may be used to treat a pathological		
CC	condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,		
CC	small cell lung, testicular or ovarian cancer, lymphoma, multiple		
XX	myeloma, neuroblastoma or acute leukemia.		

SQ Sequence 209 AA:
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1e-96;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASNLQDEFLGGLRWLYAQRMRRL 86
 1 tqdcstfghspissdfavkirelsdyllqdyptvasnlgdeelcggllwrlvlaqrwmerl 60
 DB 87 KTVAGSKMOGLERVNTIEHFVTKCAFOPPPSCLEFVOTNISRLQETSEQLVALKPWIT 146
 61 ktvagskmggllervnteihfvtkcafpppsclrfvqtnisrllqetseqvalkpwilt 120
 QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGLLLAAACGLH 206
 121 rnfscrlqlcqpdsstlppwsprrpleatapapqpllilllpvglllaaaacgh 180
 DB 207 WQTRRRTRPRGEGVPPVPSPODLLVLEH 235
 181 wqtrrrtrprgegvpvpvpspdlllveh 209

RESULT 12

AA69727
ID AAY69727 standard; Protein; 209 AA.

AC AAY69727;

DT 05-JUL-2000 (first entry)

XX Human flt-3 mutein L26F.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.

XX Homo sapiens.
OS Synthetic.

PN MO200001823-A2.

PD 13-JAN-2000.

XX 25-JUN-1999; 99WO-US14296.

XX 02-JUL-1998; 98US-0109100.

XX (IMMUNEX) IMMUNEX CORP.

XX Graddis TJ, McGrew JT;

XX WPI; 2000-182115/16.

XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 XX Claim 13; Page 82-83; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69729) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or

CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TDDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASNLQDEFLGGLRWLYAQRMRRL 86
 1 tqdcstfghspissdfavkirelsdyllqdyptvasnlgdeelcggllwrlvlaqrwmerl 60
 DB 87 KTVAGSKMOGLERVNTIEHFVTKCAFOPPPSCLEFVOTNISRLQETSEQLVALKPWIT 146
 61 ktvagskmggllervnteihfvtkcafpppsclrfvqtnisrllqetseqvalkpwilt 120
 QY 147 RQNFSCLELQCCPDSSSTLPWPSPRPLEATAPAPQPLLILLPVGLLLAAACGLH 206
 121 rnfscrlqlcqpdsstlppwsprrpleatapapqpllilllpvglllaaaacgh 180
 DB 207 WQTRRRTRPRGEGVPPVPSPODLLVLEH 235
 181 wqtrrrtrprgegvpvpvpspdlllveh 209

RESULT 13

AA69729
ID AAY69729 standard; Protein; 209 AA.

AC AAY69729;

DT 05-JUL-2000 (first entry)

XX Human flt-3 mutein A64T.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.

XX Homo sapiens.
OS Synthetic.

PN MO200001823-A2.

PD 13-JAN-2000.

XX 25-JUN-1999; 99WO-US14296.

XX 02-JUL-1998; 98US-0109100.

XX (IMMUNEX) IMMUNEX CORP.

XX Graddis TJ, McGrew JT;

XX WPI; 2000-182115/16.

XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX

PS Claim 13; Page 78-79; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1e-96; 1; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 1;

QY 27 TDGCFQHSPISSDPAVKIRELSLDYLDYPTVVASNLQDEELCGGLMRVLAQRMERL 86
DB 1 tqdcstfqhspissdflavkirelsdyllqdyprtvvasnlqdeelcgglwrlvlaqrmerl 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVLAQKPMIT 146
DB 61 ktvagskmgllervnteihftkcafpppsclrfvqtnisrlqetseqlvalkpmit 120

QY 147 RQNFSCLELQCPDSSSTLPWPSPRLPPLATAPAPQPLLLLLPVGLLLAAACWCH 206
DB 121 rqnfsclclqcpdssstlpwpssprrlpplatappppllllllpvglillaaawcch 180

QY 207 WQTRRRTPRREGQVPPVPSPODLLVHH 235
DB 181 wqtrrrtprpgeqvppvpdpqdlllvhh 209

RESULT 14
AAV69722 standard; Protein; 209 AA.
XX
AC AAV69722;
XX
XX 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein H8Y.
XX
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX

PA (IMM) IMMUNEX CORP.
XX
XX Graddis TJ, McGrew JT;
XX
DR WPI: 2000-182115/16.
XX
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 4; Page 81-82; 90pp; English.
XX
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the H8Y mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDGCFQHSPISSDPAVKIRELSLDYLDYPTVVASNLQDEELCGGLMRVLAQRMERL 86
DB 1 tqdcstfqhspissdflavkirelsdyllqdyprtvvasnlqdeelcgglwrlvlaqrmerl 60

QY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVQTNISRLQETSEQVLAQKPMIT 146
DB 61 ktvagskmgllervnteihftkcafpppsclrfvqtnisrlqetseqlvalkpmit 120

QY 147 RQNFSCLELQCPDSSSTLPWPSPRLPPLATAPAPQPLLLLLPVGLLLAAACWCH 206
DB 121 rqnfsclclqcpdssstlpwpssprrlpplatappppllllllpvglillaaawcch 180

QY 207 WQTRRRTPRREGQVPPVPSPODLLVHH 235
DB 181 wqtrrrtprpgeqvppvpdpqdlllvhh 209

RESULT 15
AAV69724 standard; Protein; 209 AA.
XX
ID AAV69724;
XX
AC AAV69724;
XX
XX 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein K84T.
XX
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS

OS Synthetic.
XX WO200001823-A2.
PN 13-JAN-2000.
XX 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
XX (IMMV) IMMUNEX CORP.
XX Graddis TJ, McGrew JT;
XX WPI; 2000-182115/16.
DR Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX Claim 4; Page 85-86; 90pp; English.
PS
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AA69720) or mature (AA69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt3-L
CC ligands and comprises the K64T mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TDGCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLQDEELCGIMRWLAQRMMERTL 86
DB 1 tqdcsfqhpsissdfavkirelsdyllqdyptvasnldgeelcgllwrlvlaqrmmertl 60

QY 87 KTYAGSKMÖGLERVNTIEHFVTKCAFQPPSCLRPVQTNISRLQETSEQLVALKPWIT 146
DB 61 ktvagskmgllervnteihfvtkcafpfpsscrlrfvqtnisrllqetseqvalkpwit 120

QY 147 RQNFSCLELOCOPDSTLRPPWSPRLATAPTAQPRLLILLIPVGLILLAAACWCH 206
DB 121 rqnfsclclqcpdssltppwsprrleataptapqppllllllpvgllllaaacwch 180

QY 207 WQTRRRTRPPGCVPPVPSQDILLVEH 235
DB 181 wqtrrrtrppgcvppvpsqdilllveh 209

RESULT 16
AA69728
ID AA69728 standard; Protein: 209 AA.
XX
AC AA69728;
XX
XX 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein L27P.

XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200001823-A2.
XX 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Graddis TJ, McGrew JT;
XX WPI; 2000-182115/16.
XX
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
XX Claim 13; Page 83-84; 90pp; English.
XX
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AA69719) or mature (AA69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt3-L
CC ligands and comprises the L27P mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.1%; Score 1107; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.9e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TDGCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLQDEELCGIMRWLAQRMMERTL 86
DB 1 tqdcsfqhpsissdfavkirelsdyllpdyptvasnldgeelcgllwrlvlaqrmmertl 60

QY 87 KTYAGSKMÖGLERVNTIEHFVTKCAFQPPSCLRPVQTNISRLQETSEQLVALKPWIT 146
DB 61 ktvagskmgllervnteihfvtkcafpfpsscrlrfvqtnisrllqetseqvalkpwit 120

QY 147 RQNFSCLELOCOPDSTLRPPWSPRLATAPTAQPRLLILLIPVGLILLAAACWCH 206
DB 121 rqnfsclclqcpdssltppwsprrleataptapqppllllllpvgllllaaacwch 180

QY 207 WQTRRRTRPPGCVPPVPSQDILLVEH 235
DB 181 wqtrrrtrppgcvppvpsqdilllveh 209

XX	RESULT 17
XX	AAV69725
ID	AAV69725 standard; Protein; 209 AA.
XX	
AC	AAV69725;
XX	
DT	05-JUL-2000 (first entry)
XX	
DE	Human flt-3 mutein W118R.
XX	
KW	Immunomodulator; immunosuppressive; cytostatic; anti-HIV;
KW	neuroprotective; antiallergic; flt3 ligand; flt3-l; wild type; allergy;
KW	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW	cellular expansion; cellular differentiation; natural killer cell;
KW	cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW	myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW	multiple myeloma; leukemia; mutein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200001823-A2.
XX	
PD	13-JAN-2000.
XX	
PF	25-JUN-1999; 99MO-US14296.
XX	
PR	02-JUL-1998; 98US-0109100.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Graddis TJ; McGrew JT;
XX	
DR	WPI; 2000-182115/16.
XX	
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT	immune response stimulation or treatment of pathological conditions
PT	contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX	
XX	Claim 4; Page 86-87; 90pp; English.
XX	
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC	which exhibits increased or decreased biological activity relative to
CC	the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC	polypeptides. This sequence represents an example of the novel flt-3
CC	ligands and comprises the W118R mutant polypeptide. The flt3-L protein
CC	binds cell surface tyrosine kinase receptors and regulate growth and
CC	differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC	be used to induce cellular expansion (especially in vivo) or
CC	differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC	cells, especially in the presence of growth factors such as interleukins,
CC	colony stimulating factors or protein kinases. The protein can also
CC	modulate, augment or enhance a patient's immune response and can be used
CC	to treat an immune disorder (e.g. allergy, autoimmunity or
CC	immunosuppression). The protein may be used to treat a pathological
CC	condition e.g. myelodysplasia, aplastic anemia, HTV infection, breast,
CC	small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC	myeloma, neuroblastoma or acute leukemia.
XX	
XX	Sequence 209 AA:
XX	
XX	Query Match 88.6%; Score 1100; DB 21; Length 209;
XX	Best Local Similarity 99.5%; Pzed. No. 8.8e-96;
XX	Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	27 TQDSFQHSISSDFAVKIRELSDYLLDQYPTVVASNIODEELCGGLRWLVLAQRWERL 86
DB	1 tqdcsfghspissdfavkirelsdylldqyptvasnlgdeelogglrwlvlaqrwerl 60
QY	87 KTVAGSAGGLERVNTETHTFVTKCAFPDPSCLEFVOTNISRLLQETSEQLVALKFWIT 146
DB	1 kTVAGSAGGLERVNTETHTFVTKCAFPDPSCLEFVOTNISRLLQETSEQLVALKFWIT 146

Db	61	ktvsgskmgqllervntelhfvtkcafgpppsclfrvtgnisrlldqetseqlvalkpkit	120
Qy	147	RQNTSRCLLELOCPDSSSTLPPEWSPRELEATAPAPOLLILLPLVGLLAAWCLH	206
Db	121	rgntsrcllelqcqgdsstllpppsprpleactapqpplllllllpyglillaaawclh	180
Qy	207	WQTRRRRTPRPEQVPVPSPDOLLVEH	235
Db	181	wqtrrrtrprpgeqvpppspqqdlllvveh	209
RESULT 18			
AAB20195			
ID	AAB20195	standard; Protein; 185 AA.	
XX			
AC	AAB20195;		
XX			
DT	14-MAY-2001	(first entry)	
XX			
DE	Human Flt-3 ligand (secreted form).		
XX			
KW	Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;		
KW	immunotherapy; therapy; tumour; cancer; melanoma; glioma;		
KW	lymphoma; autoimmune disease; infection; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	Peptide	1..26	
FT	Protein	/label= Signal_peptide	
FT		27..185	
FT		/label= Mature_protein	
XX			
PN	WO200109303-A2.		
XX			
PD	08-FEB-2001.		
XX			
PF	31-JUL-2000; 2000WO-US20679.		
XX			
PR	30-JUL-1999; 99US-0146170.		
XX			
PA	(VICAR-) VICAL INC.		
XX			
PI	Hermanson GG;		
XX			
DR	WPI: 2001-123319/13.		
DR	N-PSDB: AAF30312, AAF30314.		
XX			
PT	Immunogenic compositions comprising Flt-3 ligand encoding		
PT	polynucleotide and one or more antigen, or cytokine encoding		
PT	polynucleotides, useful for suppressing tumour growth and for		
PT	autoimmune diseases (e.g. rheumatoid arthritis) -		
XX			
XX			
PS	Claim 2; Page 138; 149pp; English.		
XX			
CC	The present sequence is that of a secreted form of human Fms-like		
CC	tyrosine kinase (Flt-3 ligand), lacking the transmembrane and		
CC	cytoplasmic domains of the full-length form (see AAB20194). This		
CC	secreted form of the Flt-3 ligand is expressed by vector VR6230		
CC	(see AAF30314). The invention is directed to enhancing the		
CC	immune response of a vertebrate to an antigen or a cytokine by		
CC	administering in vivo, into a tissue of a vertebrate, a Flt-3		
CC	ligand-encoding polynucleotide, such as VR6230, and 1 or more		
CC	antigen- or cytokine-encoding polynucleotides. The polynucleotides		
CC	are incorporated into the cells of the vertebrate in vivo, and a		
CC	prophylactically or therapeutically effective amount of Flt-3		
CC	ligand and 1 or more antigens or cytokines is produced in vivo.		
CC	Pharmaceutical compositions comprising the polynucleotides are		
CC	useful for suppressing tumour growth in a mammal. The tumour is		
CC	melanoma, glioma or lymphoma, particularly B-cell lymphoma. The		
CC	claimed pharmaceutical compositions can also be used for the		
CC	prophylactic and/or therapeutic treatment of: (a) bacterial (e.g.		
CC	Bacillus infections), viral (e.g. hepatitis B and C in humans),		
CC			

CC parasitic (e.g. malaria) and fungal infections; (b) autoimmune
 CC diseases (e.g. rheumatoid arthritis and osteoarthritis); (c)
 CC cancer; and (d) Aujeszky's disease in pigs. Various other examples
 CC of these diseases are given in the specification.

XX Sequence 185 AA;

Query Match 78.1%; Score 970; DB 22; Length 185;
 Best Local Similarity 99.5%; Pred. No. 1.4e-83;
 Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
 Db 1 mtvlapawspptylllllllsglsgtqdcsfqhspsidpavkirelsdyllqdyptv 60

QY 61 ASNODELGGMLRVLTAQRWMERLKTVAAGSKMOGLLEVRNTEIHVYTKCAFQPPSCL 120
 Db 61 asnlqdeclgcalwrlvlaqrwmerlktvagskmqgllevrnteihvltkcafpppscl 120

QY 121 RFVQNTISRLOETSEOLVALKPWTRQNFSCLELOCCPDSSSTLPMPSPRELEATAPT 180
 Db 121 rfvgntisrllqetseqvalkpwttrqntsrclclqcgpdssstlppmpsprleatapt 180

QY 181 APQPP 185
 Db 181 apqpp 185

RESULT 19
 AAY58204
 ID AAY58204 standard; Protein; 294 AA.

XX AAY58204;
 DT 14-MAR-2000 (first entry)

XX Canine Flt-3 ligand.
 DE Canine Flt-3 ligand.
 XX Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.
 XX WO9961618-A2.

XX 02-DEC-1999.
 PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.
 PF 28-MAY-1999; 99WO-US11942.
 XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.
 PA (HESK-) HESKA CORP.
 XX
 PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.
 DR N-PSDB; AAZ55487, AAZ55488, AAZ55489, AAZ55490.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 3b; Page 159-160; 264pp; English.

XX Sequences AAY58204 and AAY58206-Y58209 respectively represent
 CC encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
 CC sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
 CC ligand. The invention relates to canine interleukin-4 (IL-4),
 CC canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, and nucleotides associated

CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX Sequence 294 AA;

Query Match 72.1%; Score 895.5; DB 21; Length 294;
 Best Local Similarity 77.1%; Pred. No. 2.6e-76;
 Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

QY 1 MTVLAPAMSPPTYYLLLLLSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
 Db 1 mtvlapawspptylllllllsglsgtqdcsfqhspsidpavkirelsdyllqdyptv 60

QY 61 ASNODELGGMLRVLTAQRWMERLKTVAAGSKMOGLLEVRNTEIHVYTKCAFQPPSCL 120
 Db 61 asnlqdeclgcalwrlvlaqrwmerlktvagskmqgllevrnteihvltkcafpppscl 120

QY 121 RFVQNTISRLOETSEOLVALKPWTRQNFSCLELOCCPDSSSTLPMPSPRELEATAPT 180
 Db 121 rfvgntisrllqetseqvalkpwttrqntsrclclqcgpdssstlppmpsprleatapt 180

QY 181 APQPP-LLLLLLLPYGLLLAAAWCLHW-QRTRRTPPGSGQVPPVS----PQD 229
 Db 181 apqpprlllllllpvaylllmstawclhwrrrrrrrpygqgrtlrpsershlped 236

RESULT 20
 AAY58210
 ID AAY58210 standard; Protein; 291 AA.

XX AAY58210;
 DT 14-MAR-2000 (first entry)

XX Feline Flt-3 ligand.
 DE Feline Flt-3 ligand.

XX Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.
 XX Fells catus.

XX WO9961618-A2.
 PN WO9961618-A2.

XX 02-DEC-1999.
 PD 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US11942.
 PF 28-MAY-1999; 99WO-US11942.
 XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.
 PA (HESK-) HESKA CORP.
 XX
 PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/05.
 DR N-PSDB; AAZ55518, AAZ55519, AAZ55520, AAZ55521.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 3c; Page 186-187; 264pp; English.
 XX Sequences AAY58204 and AAY58206-Y58209 respectively represent


```
RESULT 24
AA58211
ID AAY58211 standard; Protein; 265 AA.
XX
AC AAY58211;
XX
DT 14-MAR-2000 (first entry)
XX
DE Feline mature Flt-3 ligand.
XX
KW Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
KM immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Fells catus.
XX
PN WO961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR / 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Dreltz MJ, Wonderling RS;
XX
DR N-PSDB; AA55522, AA55523.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 3c: Page 191-192; 264pp; English.
XX
CC Sequences AAY58204 and AAY58206-Y58209 respectively represent
CC encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
CC sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
CC ligand. The invention relates to canine interleukin-4 (IL-4),
CC canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense
CC oligonucleotides). The proteins may be used to raise antibodies and to
CC screen for modulators of activity, while the antibodies may be used in
CC detection, and in drug targeting.
XX
SQ Sequence 265 AA;
XX
Query Match 63.7%; Score 791.5; DB 21; Length 265;
Best Local Similarity 80.8%; Pred. No. 1.5e-66;
Matches 156; Conservative 8; Mismatches 28; Indels 1; Gaps 1;
```

```
QY 149 NFSRCLELCQDPDSSSTLPPEPMSRPLEXTAPAPQPP-LLILLLLPYGLLLAAACLIHW 207
DB 123 nISgcLeIqcqdpdsstlpIprspraleataIpapqapIlliIlliIImSaawcIhw 182
QY 208 ORTRRRTPRPGQ 220
DB 183 rrrrrwrrpyprqg 195
```

```
RESULT 25
AAR67540
ID AAR67540 standard; Protein; 231 AA.
XX
AC AAR67540;
XX
DT 05-AUG-1995 (first entry)
XX
DE Mouse flt-3 ligand.
XX
KW Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Peptide 1..27
FT /label= Sig_peptide
FT /label= Extracellular_domain
FT /label= Transmembrane_domain
FT /label= Cytoplasmic_domain
XX
PN EP627487-A.
XX
PD 07-DEC-1994.
XX
PF 19-MAY-1994; 94EP-0303575.
XX
PR 24-MAY-1993; 93US-0068394.
PR 12-AUG-1993; 93US-0106463.
PR 25-AUG-1993; 93US-0111758.
PR 03-DEC-1993; 93US-0162407.
PR 11-MAR-1994; 94US-0209502.
PR 11-MAY-1994; 94US-0243545.
XX
PA (IMM) IMMUNEX CORP.
XX
PI Beckmann MP, Lyman SD;
XX
DR MPI: 1995-008071/02.
XX
DR N-PSDB; AAG79076.
XX
PT Isolated ligands for flt 3 receptors - useful for treating
PT anaemia, AIDS and various cancers
XX
PS Disclosure; Page 25-27; 33pp; English.
XX
CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a
CC cDNA library of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells
CC using a slide autoradiography method. Flt3-L stimulates
CC production of progenitor and stem cells, and can be used e.g.
CC in gene therapy protocols.
XX
SQ Sequence 231 AA;
XX
Query Match 61.9%; Score 768.5; DB 16; Length 231;
Best Local Similarity 70.3%; Pred. No. 1.9e-64;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

Tue Aug 6 09:34:29 2002

us-09-448-378-1.ray

Page 16

[illegible]

Search completed: August 6, 2002, 09:39:02
Job time: 293 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:37:59 ; Search time 201.6 Seconds

(without alignments)
410,295 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MYTLAPANSPTITLLLLLL.....RREGEVPPVSPQDLIVRH 235

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 3502263 segs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCPNUS_COMB.pep:*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
- 14: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
- 15: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
- 16: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
- 17: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
- 18: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
- 19: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
- 20: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
- 21: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
- 22: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
- 23: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
- 24: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
- 25: /cgn2_6/ptodata/2/paa/US102_COMB.pep:*
- 26: /cgn2_6/ptodata/2/paa/US103_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1	PCT-US98-12085-4
2	1242	100.0	235	5	US-08-106-463-6
3	1242	100.0	235	5	US-08-111-758-6
4	1242	100.0	235	5	US-08-162-407-6
5	1242	100.0	235	8	US-08-444-625-6
6	1242	100.0	235	8	US-08-444-626-6
7	1242	100.0	235	8	US-08-444-632-6

8	1242	100.0	235	10	US-08-669-692-6	Sequence 6, Appli
9	1242	100.0	235	12	US-08-877-421-4	Sequence 4, Appli
10	1242	100.0	235	18	US-09-448-378-1	Sequence 1, Appli
11	1242	100.0	235	20	US-09-629-430B-19	Sequence 19, Appli
12	1242	100.0	235	22	US-09-891-498-4	Sequence 4, Appli
13	1242	100.0	235	23	US-09-904-536-1	Sequence 1, Appli
14	1242	100.0	235	23	US-09-983-806-6	Sequence 6, Appli
15	1242	100.0	235	24	US-10-095-449-6	Sequence 6, Appli
16	1237	99.6	235	22	US-09-891-498-5	Sequence 5, Appli
17	1236	99.5	235	5	US-08-155-111-34	Sequence 34, Appli
18	1236	99.5	235	5	US-08-162-413-34	Sequence 34, Appli
19	1236	99.5	235	6	US-08-261-553-34	Sequence 34, Appli
20	1236	99.5	235	8	US-08-472-168-34	Sequence 34, Appli
21	1236	99.5	235	8	US-08-484-882-34	Sequence 34, Appli
22	1236	99.5	235	8	US-08-486-661-34	Sequence 34, Appli
23	1236	99.5	235	20	US-09-629-430B-23	Sequence 23, Appli
24	1124	90.5	212	23	US-09-904-536-10	Sequence 10, Appli
25	1114	89.7	209	13	US-08-955-090-145	Sequence 145, App
26	1114	89.7	209	23	US-09-904-536-18	Sequence 18, Appli
27	1110	89.4	209	23	US-09-904-536-9	Sequence 9, Appli
28	1110	89.4	209	23	US-09-904-536-12	Sequence 12, Appli
29	1110	89.4	209	23	US-09-904-536-14	Sequence 14, Appli
30	1110	89.4	209	23	US-09-904-536-17	Sequence 17, Appli
31	1108	89.2	209	23	US-09-904-536-11	Sequence 11, Appli
32	1108	89.2	209	23	US-09-904-536-15	Sequence 15, Appli
33	1107	89.1	209	23	US-09-904-536-13	Sequence 13, Appli
34	1106	89.0	209	23	US-09-904-536-8	Sequence 8, Appli
35	1100	88.6	209	23	US-09-904-536-16	Sequence 16, Appli
36	992	79.9	199	21	US-09-757-027-671	Sequence 671, App
37	970	78.1	185	20	US-09-629-430B-24	Sequence 24, Appli
38	963	77.5	189	22	US-09-891-498-2	Sequence 2, Appli
39	895.5	72.1	294	17	US-09-322-409-7	Sequence 7, Appli
40	895.5	72.1	294	18	US-09-451-527-7	Sequence 7, Appli
41	894.5	72.0	291	17	US-09-322-409-44	Sequence 44, Appli
42	894.5	72.0	291	18	US-09-451-527-44	Sequence 44, Appli
43	834	67.1	178	20	US-09-629-430B-21	Sequence 21, Appli
44	797.5	64.2	268	17	US-09-322-409-23	Sequence 23, Appli
45	797.5	64.2	268	18	US-09-451-527-23	Sequence 23, Appli
46	796.5	64.1	276	17	US-09-322-409-26	Sequence 26, Appli
47	796.5	64.1	276	18	US-09-451-527-26	Sequence 26, Appli
48	791.5	63.7	265	17	US-09-322-409-49	Sequence 49, Appli
49	791.5	63.7	265	18	US-09-451-527-49	Sequence 49, Appli
50	768.5	61.9	231	1	PCT-US98-12085-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US98-12085-4
Sequence 4, Application PC/TUS9812085
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 31 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, Version 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2855-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US98-12085-4

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVALPAMSPPTTYLLILLSSLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLODEELCGGLRWLVLAQRMERLKTAVAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
DB 61 ASNLODEELCGGLRWLVLAQRMERLKTAVAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
QY 121 REVQTNISRLQETSEQVALKFWITRQNFSCLELQCCOPDSSSTLPPWSPRPLEATPT 180
DB 121 REVQTNISRLQETSEQVALKFWITRQNFSCLELQCCOPDSSSTLPPWSPRPLEATPT 180
QY 181 APOPELLLLLPYGLLLAAACLIHQRTRRTPRGEQVPPVPSQDILLVEH 235
DB 181 APOPELLLLLPYGLLLAAACLIHQRTRRTPRGEQVPPVPSQDILLVEH 235

RESULT 2

US-08-106-463-6

Sequence 6, Application US/08106463

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/106,463

FILING DATE: 19930812

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-106-463-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLILLSSLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVALPAMSPPTTYLLILLSSLSGSGTODCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLODEELCGGLRWLVLAQRMERLKTAVAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
DB 61 ASNLODEELCGGLRWLVLAQRMERLKTAVAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
QY 121 REVQTNISRLQETSEQVALKFWITRQNFSCLELQCCOPDSSSTLPPWSPRPLEATPT 180
DB 121 REVQTNISRLQETSEQVALKFWITRQNFSCLELQCCOPDSSSTLPPWSPRPLEATPT 180
QY 181 APOPELLLLLPYGLLLAAACLIHQRTRRTPRGEQVPPVPSQDILLVEH 235
DB 181 APOPELLLLLPYGLLLAAACLIHQRTRRTPRGEQVPPVPSQDILLVEH 235

RESULT 3

US-08-111-758-6

Sequence 6, Application US/08111758

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/111,758

FILING DATE: August 25, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-111-758-6

Query Match 100.0%; Score 1242; DB 5; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPPTYYLLLLLSGLSGTODCSFOHSPISSDFAVKIRELSDYLLQDYPTV 60
DB 1 MTVALAPAMSPPTYYLLLLLSGLSGTODCSFOHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNIQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLERVNTTEIHVTKCAFQPPSCL 120
DB 61 ASNIQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLERVNTTEIHVTKCAFQPPSCL 120
QY 121 RFVQNTISRLQETSEQLVALKPWITRONFSRCLLELQCPDSSSTLPPMSPRPLEATAPT 180
DB 121 RFVQNTISRLQETSEQLVALKPWITRONFSRCLLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APOPELLLLLLPVGLLLAAWCLHMORTRRRPPRGEQVPVPSPQDLLVEH 235
DB 181 APOPELLLLLLPVGLLLAAWCLHMORTRRRPPRGEQVPVPSPQDLLVEH 235

RESULT 4

US-08-162-407-6
; Sequence 6, Application US/08162407
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-407-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPPTYYLLLLLSGLSGTODCSFOHSPISSDFAVKIRELSDYLLQDYPTV 60
DB 1 MTVALAPAMSPPTYYLLLLLSGLSGTODCSFOHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNIQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLERVNTTEIHVTKCAFQPPSCL 120
DB 61 ASNIQDEELCGGLMRLVLAQRMERLKTVAAGSKMGLERVNTTEIHVTKCAFQPPSCL 120
QY 121 RFVQNTISRLQETSEQLVALKPWITRONFSRCLLELQCPDSSSTLPPMSPRPLEATAPT 180
DB 121 RFVQNTISRLQETSEQLVALKPWITRONFSRCLLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APOPELLLLLLPVGLLLAAWCLHMORTRRRPPRGEQVPVPSPQDLLVEH 235
DB 181 APOPELLLLLLPVGLLLAAWCLHMORTRRRPPRGEQVPVPSPQDLLVEH 235

RESULT 5

US-08-444-625-6
; Sequence 6, Application US/08444625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,625
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-625-6

Query Match 100.0%; Score 1242; DB 8; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
Db 1 MTVALPAMSPPTTYLLLLLLSSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
QY 61 ASNIODEELCGGLMRVLQRMERKTVAGSKMGLERNTLHVTCAQPPPSCL 120
Db 61 ASNIODEELCGGLMRVLQRMERKTVAGSKMGLERNTLHVTCAQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDPSSTLPWPSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDPSSTLPWPSPRPLEATAPT 180
QY 181 APOPPILLLLLPVGLLLAAACLMWORTRRRPRPEQYPPVPSPODLLVYH 235
Db 181 APOPPILLLLLPVGLLLAAACLMWORTRRRPRPEQYPPVPSPODLLVYH 235

RESULT 6

US-08-444-626-6
; Sequence 6, Application US/08444626

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-626-6

Query Match 100.0%; Score 1242; DB 8; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
Db 1 MTVALPAMSPPTTYLLLLLLSSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
QY 61 ASNIODEELCGGLMRVLQRMERKTVAGSKMGLERNTLHVTCAQPPPSCL 120
Db 61 ASNIODEELCGGLMRVLQRMERKTVAGSKMGLERNTLHVTCAQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDPSSTLPWPSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDPSSTLPWPSPRPLEATAPT 180
QY 181 APOPPILLLLLPVGLLLAAACLMWORTRRRPRPEQYPPVPSPODLLVYH 235
Db 181 APOPPILLLLLPVGLLLAAACLMWORTRRRPRPEQYPPVPSPODLLVYH 235

RESULT 7

US-08-444-632-6
; Sequence 6, Application US/08444632

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,632
FILING DATE: 19-MAY-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-444-632-6

Query Match	100.0%;	Score 1242;	DB 8;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2.6e-102;		
Matches 235; Conservative	0;	Mismatches	0;	Gaps 0

Oy	1	MTVAPAMSPPTTYLLLLLLSSSGISGQDCFSQHSPISSDFAVKIRLSLDYLLDDYVTV	60
Db	1	MTVAPAMSPPTTYLLLLLLSSSGISGQDCFSQHSPISSDFAVKIRLSLDYLLDDYVTV	60
Oy	61	ASNLODELCCGLMRVLVAQRMERLTKVAGSKQGGLLERNTEIHEVTCAFOPPSCL	120
Db	61	ASNLODELCCGLMRVLVAQRMERLTKVAGSKQGGLLERNTEIHEVTCAFOPPSCL	120
Oy	121	RFGVNISRRLQETSEGVVALKPWITRQNFSCRLELCOPDSSLTLPMPWSRPLEATAPT	180
Db	121	RFGVNISRRLQETSEGVVALKPWITRQNFSCRLELCOPDSSLTLPMPWSRPLEATAPT	180
Oy	181	AQPPLLLLLLLLPGGLLLAAMCLHMQRTRRRTPRGEGVPVPYSQDLLLVEN	235
Db	181	AQPPLLLLLLLLPGGLLLAAMCLHMQRTRRRTPRGEGVPVPYSQDLLLVEN	235

RESULT 8

US-08-669-692-6

```

1 Sequence 6, Application us/08669692
2 GENERAL INFORMATION:
3 APPLICANT: Lyman, Stewart D.
4 APPLICANT: Beckmann, M. Patricia
5 TITLE OF INVENTION: Ligands for fli3/fli-2 Receptors
6 NUMBER OF SEQUENCES: 8
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
9 STREET: 51 University Street
10 CITY: Seattle
11 STATE: Washington
12 COUNTRY: US
13 ZIP: 98101
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: Apple Macintosh
17 OPERATING SYSTEM: Macintosh 7.0.1
18 SOFTWARE: Microsoft Word, Version #5.1
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/669,692
21 FILING DATE: 24-JUN-1996
22 CLASSIFICATION: 530
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US/08/162,407
25 FILING DATE: December 3, 1993
26 APPLICATION NUMBER: 08/111,758
27 FILING DATE: August 25, 1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 08/106,463
30 FILING DATE: August 12, 1993
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 08/068,394
33 FILING DATE: May 24, 1993
34 CLASSIFICATION: 530
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Malaska, Stephen L.
37 REGISTRATION NUMBER: 32,655
38 REFERENCE/DOCKET NUMBER: 2813-C
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (206) 587-0430
41 TELEFAX: (206) 233-0644
42 TELEX: 756822
43 INFORMATION FOR SEQ. ID NO: 6:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 235 amino acids
46 TYPE: amino acid
47 TOPOLOGY: linear
48

```

```

; MOLECULE TYPE: protein
US-08-669-692-6

```

Query Match	100.0%;	Score 1242;	DB 10;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2.6e-102;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTVLAPAMSPPTTYLLLLLLLLSSGSLGSDGSCFQHSPISSDFAVKIRELSDYLLADYVTV	60
Db	1	MTVLAPAMSPPTTYLLLLLLLLSSGSLGSDGSCFQHSPISSDFAVKIRELSDYLLADYVTV	60
QY	61	ASNLODELGGIMRLVLAQSMMERIKTVASGKMGILERNTREIHYTVKAFQPPSCL	120
Db	61	ASNLODELGGIMRLVLAQSMMERIKTVASGKMGILERNTREIHYTVKAFQPPSCL	120
QY	121	RFVQTNISRLQETSEQLVALKPMITTRQNFSCRLQACQPPSSITLPPWSPRLPEATAPT	180
Db	121	RFVQTNISRLQETSEQLVALKPMITTRQNFSCRLQACQPPSSITLPPWSPRLPEATAPT	180
QY	161	APQPLLILLILLPVGLILLAAACLIHMORTRRRPGRGEVPPVPSQDILLVH	235
Db	161	APQPLLILLILLPVGLILLAAACLIHMORTRRRPGRGEVPPVPSQDILLVH	235

RESULT

US-08-877-421-4

```

: Sequence 4, Application US/08877421
:
: GENERAL INFORMATION:
:
: APPLICANT: Viney, Joanne L.
: APPLICANT: Mowatt, Allan MCI.
: APPLICANT: Abbott, Nicholas
: TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation
: STREET: 51 University Street
:
: CITY: Seattle
:
: STATE: Washington
:
: COUNTRY: US
:
: ZIP: 98101
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Macintosh 7.6
: SOFTWARE: Microsoft Word, Version #6.0.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/877,421
: FILING DATE: 17-JUN-1997
:
: CLASSIFICATION: 514
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Malaska, Stephen L.
: REGISTRATION NUMBER: 32,655
: REFERENCE/DOCKET NUMBER: 2855
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (206) 587-0430
:
: TELEFAX: (206) 233-0644
:
: TELEX: 756822
:
: INFORMATION FOR SEQ ID NO: 4:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 235 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-877-421-4

```

Query Match	100.0%;	Score 1242;	DB 12;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2.0e-102;		
Matches 235; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTVLPAHNSPTTYLLLLLLISGSLGTDCCSQHSHPISSDFAVKTRRELSDYLLQDYPYTV	60	

```
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235

RESULT 10
US-09-448-378-1
; Sequence 1, Application US/09448378
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 18; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235

RESULT 11
US-09-629-430B-19
; Sequence 19, Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-629-430B-19
```

```
Query Match 100.0%; Score 1242; DB 20; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235

RESULT 12
US-09-891-498-4
; Sequence 4, Application US/09891498
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: C1001244
; CURRENT APPLICATION NUMBER: US/09/891,498
; CURRENT FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
US-09-891-498-4

Query Match 100.0%; Score 1242; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
Db 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGGLEERVNTEIHFTVCARPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLLAAMCLHWQRTRRTPRPEQVPPVPSQDILLVEH 235

RESULT 13
US-09-904-536-1
; Sequence 1, Application US/09904536
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
```

CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-1

Query Match 100.0%; Score 1242; DB 23; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
DB 1 MTVALPAMSPPTTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRVLAQRMMERLKTIVAGSKMOGLERVNTETIHFYTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLAQRMMERLKTIVAGSKMOGLERVNTETIHFYTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APQPELLLLLPVGLLLAAWCLHMORTRRTPRPGQVPVPSPDILLVH 235
DB 181 APQPELLLLLPVGLLLAAWCLHMORTRRTPRPGQVPVPSPDILLVH 235

RESULT 14
US-09-983-806-6
Sequence 6, Application US/09983806
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 23; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
DB 1 MTVALPAMSPPTTYLLLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRVLAQRMMERLKTIVAGSKMOGLERVNTETIHFYTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLAQRMMERLKTIVAGSKMOGLERVNTETIHFYTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APQPELLLLLPVGLLLAAWCLHMORTRRTPRPGQVPVPSPDILLVH 235
DB 181 APQPELLLLLPVGLLLAAWCLHMORTRRTPRPGQVPVPSPDILLVH 235

RESULT 15
US-10-095-449-6
Sequence 6, Application US/10095449
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 24; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
DB 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
QY 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
DB 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235
DB 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235

RESULT 16
US-09-891-498-5
Sequence 5, Application US/09891498
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01244
CURRENT APPLICATION NUMBER: US/09/891,498
CURRENT FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 235
TYPE: PROT
ORGANISM: Human
US-09-891-498-5

Query Match 99.6%; Score 1237; DB 22; Length 235;
Best Local Similarity 99.6%; Pred. No. 7,4e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
DB 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
QY 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
DB 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235
DB 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235

DB 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235

RESULT 17
US-08-155-111-34
Sequence 34, Application US/08155111
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands;
TITLE OF INVENTION: Agonists; Antagonists
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,111
FILING DATE: 19-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-155-111-34

Query Match 99.5%; Score 1236; DB 5; Length 235;
Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
DB 61 ASNIODELDCGLMRLVLAQRMERLKTVAAGSMOGLERVTETIHFYTKCAFQPPPSCL 120
QY 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
DB 121 REVQTNISRLQETSEQVALKPKWITRONFSRCLIEQCOPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235
DB 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRGQVPPVPSPODLLLVEH 235

RESULT 18
US-08-162-413-34
Sequence 34, Application US/08162413
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.

APPLICANT: Lee, Frank D.
US-08-261-553-34
SEQUENCE 34, Application US/08261553
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,413
FILING DATE: 03-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-413-34

Query Match 99.5%; Score 1236; DB 5; Length 235;
Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYVTV 60
DB 1 MTVLAPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYVTV 60
QY 61 ASNLODEELCGALMRLVLAQRMMERLKTVAAGSKMOGLIERVNEIHVFYKCAFPSPSCL 120
DB 61 ASNLODEELCGALMRLVLAQRMMERLKTVAAGSKMOGLIERVNEIHVFYKCAFPSPSCL 120
QY 121 RFOVQINISRLQETSEQLVALKFWITRONFSRCLFELQCPDSSSTLPPMPSPPLEATAPT 180
DB 121 RFOVQINISRLQETSEQLVALKFWITRONFSRCLFELQCPDSSSTLPPMPSPPLEATAPT 180
QY 181 APOPELLLLLLLVGLLLAAAWCLMORTRRRTPRPGEOVPPVPSQOLLVEH 235
DB 181 APOPELLLLLLLVGLLLAAAWCLMORTRRRTPRPGEOVPPVPSQOLLVEH 235

RESULT 19
US-08-261-553-34
SEQUENCE 34, Application US/08261553
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,553
FILING DATE: 17-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-553-34

Query Match 99.5%; Score 1236; DB 6; Length 235;
Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYVTV 60
DB 1 MTVLAPAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYVTV 60
QY 61 ASNLODEELCGALMRLVLAQRMMERLKTVAAGSKMOGLIERVNEIHVFYKCAFPSPSCL 120
DB 61 ASNLODEELCGALMRLVLAQRMMERLKTVAAGSKMOGLIERVNEIHVFYKCAFPSPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCLELQCCQPDSSSTLPPEWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCLELQCCQPDSSSTLPPEWSPRPLEATAPT 180
QY 181 APQPLLILLPLVGLLLLAAMCLHWQRTTRRRPRGEOVPPVPSQDILLVEH 235
Db 181 APQPLLILLPLVGLLLLAAMCLHWQRTTRRRPRGEOVPPVPSQDILLVEH 235

RESULT 20

US-08-472-168-34
Sequence 34, Application US/08472168
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,168
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,553
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9156
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-168-34

Query Match

99.5%; Score 1236; DB 8; Length 235;

Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTVYLLILLSSGSLGTDCCSPHSPISSDPAVKIRLSDYLDYPTV 60
Db 1 MTVLAPAMSPPTVYLLILLSSGSLGTDCCSPHSPISSDPAVKIRLSDYLDYPTV 60
QY 61 ASNLQDEELGGLNRLVLAQRMERLKTIVAGSKMGLLERYNTEIHFTKCAFQPPSCL 120
Db 61 ASNLQDEELGGLNRLVLAQRMERLKTIVAGSKMGLLERYNTEIHFTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCLELQCCQPDSSSTLPPEWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCLELQCCQPDSSSTLPPEWSPRPLEATAPT 180
QY 181 APQPLLILLPLVGLLLLAAMCLHWQRTTRRRPRGEOVPPVPSQDILLVEH 235
Db 181 APQPLLILLPLVGLLLLAAMCLHWQRTTRRRPRGEOVPPVPSQDILLVEH 235

RESULT 21

US-08-484-882-34
Sequence 34, Application US/08484882
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,553
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7GD
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-882-34

Query Match 99.5%; Score 1236; DB 8; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 QY 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235

RESULT 22

US-08-486-661-34
 Sequence 34, Application US/08486661
 GENERAL INFORMATION:
 APPLICANT: Hannum, Charles H.
 APPLICANT: Culpepper, Janice A.
 APPLICANT: Lee, Frank D.
 APPLICANT: Birnbaum, Daniel
 TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
 TITLE OF INVENTION: AGONISTS; ANTAGONISTS
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,661
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0350K7GC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-661-34

Query Match 99.5%; Score 1236; DB 8; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 QY 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235

RESULT 23

US-09-629-430B-23
 Sequence 23, Application US/09629430B
 GENERAL INFORMATION:
 APPLICANT: Hermanson, Gary George
 TITLE OF INVENTION: FLT-3-ligand-Encoding Polynucleotide as a
 FILE REFERENCE: 1530.0130001
 CURRENT APPLICATION NUMBER: US/09/629,430B
 CURRENT FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 60/146,170
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 23
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-629-430B-23

Query Match 99.5%; Score 1236; DB 20; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLDDYPYTV 60
 QY 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELCGLMRLVLAQRMERLKTVAAGSKMGGLLERNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHMQRTRRRPRGEOVPVPVPSQDILLVH 235

RESULT 24

US-09-904-536-10
 Sequence 10, Application US/09904536
 GENERAL INFORMATION:
 APPLICANT: Graddis, Thomas J.
 APPLICANT: McGrew, Jeffrey T.
 TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 FILE REFERENCE: 03260.0028

; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-904-536-10

Query Match 90.5%; Score 1124; DB 23; Length 212;
Best Local Similarity 100.0%; Pred. No. 8.1e-92;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 SGTDGCFQHSPISSDFAVKIRELSDYLLDDYPTVASNLQDEBELGGLMRLVLAQRME 84
DB 2 SGTDDCFQHSPISSDFAVKIRELSDYLLDDYPTVASNLQDEBELGGLMRLVLAQRME 61
QY 85 RLKTVAGSKMOGLLERYNTEIHFTKCAFPSPCLRFVOTNISRLLOETSEOLVALKPM 144
DB 62 RLKTVAGSKMOGLLERYNTEIHFTKCAFPSPCLRFVOTNISRLLOETSEOLVALKPM 121
QY 145 ITRQNFSCLELQCPDPSSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAAMC 204
DB 122 ITRQNFSCLELQCPDPSSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAAMC 181
QY 205 LHMORTRRTPRGEQVPPVPSQDILLVEH 235
DB 182 LHMORTRRTPRGEQVPPVPSQDILLVEH 212

RESULT 25
US-08-955-090-145
; Sequence 145, Application US/08955090
; GENERAL INFORMATION:
; APPLICANT: Mc Wherter, Charles
; APPLICANT: Feng, Yiqing
; APPLICANT: Mc Kearn, John
; APPLICANT: Staten, Nicholas
; APPLICANT: Streeter, Philip
; APPLICANT: Woulfe, Susan
; APPLICANT: Minsterly, Nancy
; TITLE OF INVENTION: Novel fit3 Receptor Agonists
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: G. D. Searle Corporate Patent Department
; STREET: P.O. Box 55110
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,090
; FILING DATE: 21-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,094
; FILING DATE: 25-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2993/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-737-6986

; TELEFAX: 314-737-6972
; TELEX:
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 209 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
US-08-955-090-145

Query Match 89.7%; Score 1114; DB 13; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.3e-91;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 TODCSFQHSPISSDFAVKIRELSDYLLDDYPTVASNLQDEBELGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSDYLLDDYPTVASNLQDEBELGGLMRLVLAQRMERL 60
QY 87 KTVAGSKMOGLLERYNTEIHFTKCAFPSPCLRFVOTNISRLLOETSEOLVALKPMIT 146
DB 61 KTVAGSKMOGLLERYNTEIHFTKCAFPSPCLRFVOTNISRLLOETSEOLVALKPMIT 120
QY 147 RQNFSCLELQCPDPSSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACLN 206
DB 121 RQNFSCLELQCPDPSSTLPPWSPRPLEATAPAPQPLLILLPVGLLLAAACLN 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRGEQVPPVPSQDILLVEH 209

Search completed: August 6, 2002, 09:44:48
Job time: 409 sec

Tue Aug 6 09:34:31 2002

us-09-448-378-1.ram

Page 13


```

; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-368-263-1

Query Match          100.0%; Score 1242; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 5,5e-98;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
DB 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 235
DB 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 235

RESULT 3
PCT-US02-20172-5
; Sequence 5, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-5

Query Match          99.6%; Score 1237; DB 1; Length 235;
Best Local Similarity 99.6%; Pred. No. 1,5e-97;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
DB 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
```

```

QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 235
DB 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 235

RESULT 4
PCT-US02-20172-2
; Sequence 2, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-2

Query Match          77.5%; Score 963; DB 1; Length 189;
Best Local Similarity 80.4%; Pred. No. 2,3e-74;
Matches 189; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

QY 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMOGLLEEVNTEIHFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
DB 121 REVQTNISRLQETSEQLVALKFWITRONFSRCLELOCQDSSSTLPPEWSPRPLEATAP 180
DB 115 -----DSSSTLPPEWSPRPLEATAP 134

QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 235
DB 135 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSQDILLVEH 189

RESULT 5
US-10-053-355A-1
; Sequence 1, Application US/10053355A
; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High
; TITLE OF INVENTION: Small Molecule Drug Discovery
; FILE REFERENCE: A-70882/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/053,355A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/316,723
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-355A-1

Query Match          66.2%; Score 822; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,8e-62;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNLODEELCGGLMRLVLAQRMMERL 86
```

```

US-60-391-781-1122

Query Match
Best Local Similarity 32.9%; Score 97; DB 7; Length 637;
Matches 28; Conservative 8; Mismatches 25; Indels 24; Gaps 4;

QY 162 SSTLPSPMSRPLEATAPPA-PQPLLLLLPVGLLLIAA-----WCLHWQTRRRRT 214
      11:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 16 STSPSPMSASIQATASASRPDP-----PGTTTSATATPTPRMPLPSSASVSRA 68

QY 215 PRGEQVPP-----VPSPOD 229
      11:||||
DB 69 TSPGHCIPLLRASAAAAVPAAPGD 93

RESULT 8
US-09-935-625-5799
; Sequence 5799, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPAB
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 5799
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..671
; OTHER INFORMATION: Ceres Seq. ID no. 30711413
US-09-935-625-5799

Query Match
Best Local Similarity 27.7%; Score 95.5; DB 5; Length 671;
Matches 31; Conservative 14; Mismatches 28; Indels 39; Gaps 5;

QY 138 LVALKPWITRONFSRCLL--QCQPD-----SSTLPSPMSPR 172
      11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 195 LVQCTPDLTRDDCSRCIQLVINQIPTDRIGARINPSCSTRYEIYAFYTESAVPP--PP 252

QY 173 PLEATAPPAQPP-----LLLLLP--VGLLLIAAWCLHWQTRRR 212
      11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 253 PPSISTPVSAPPRSGDKGNSKVLVIAIVPIYAVLLFIAGYCFLTRARRK 304

RESULT 9
US-60-382-898-359
; Sequence 359, Application US/60382898
; GENERAL INFORMATION:
; APPLICANT: Hudson, Keith
; APPLICANT: et al.
; TITLE OF INVENTION: Plant Receptors and Ligands
; FILE REFERENCE: 1066P
; CURRENT APPLICATION NUMBER: US/60/382,898
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 1344
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(658)
; OTHER INFORMATION: xaa = Any Amino Acid
; US-60-382-898-359

```


LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-21694-15

Query Match 7.1%; Score 88.5; DB 1; Length 579;
Best Local Similarity 21.8%; Pred. No. 21;
Matches 48; Conservative 20; Mismatches 69; Indels 83; Gaps 7;

QY 4 LAPAMPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRLSLDYLDYPTVAVSN 63
DB 289 LEPDMG--NYLDGLLLIADKLOG---PFSEFLTAESIGVKISEGLMYLQENSAAVSAQV 342
QY 64 LOD-----EELCGLMRLVLAQRMRERLKTAVAGSKMOGLLERVNTIEH 106
DB 343 FOECGPDPVPARNRRAPPREAGRLWSMVTSE--ERPTTAAG-----384
QY 107 FVTKCAFQPPPCSLRFVQPNISRLLOETSEOLVALKPMITRONFSRCLQCOQPDST-- 164
DB 385 -----TNLRLVWELERLARMRGFWARLSLIVCGDSRMAADASLEA 426
QY 165 -----LPPWSPRPLE-----ATAPTAP 182
DB 427 APCWTGAGRGRLPLPVYGGSPAEOYNNPELKYDASGDPVP 466

RESULT 16
US-10-155-881-31529
Sequence 31529, Application US/10155881
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Lufiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 31529
LENGTH: 612
TYPE: PRT
ORGANISM: zea mays
US-10-155-881-31529

Query Match 7.1%; Score 88.5; DB 6; Length 612;
Best Local Similarity 29.7%; Pred. No. 22;
Matches 27; Conservative 6; Mismatches 23; Indels 35; Gaps 3;

QY 131 LQETSOVALKPMITRONFSRCLQCOQPDSTLP---PMSPPLEATAPTAQPPL 186
DB 274 LPMSSSLMADSDW-----RSLKVQWDEPSSILRPDRISFWEVEPLDANPQSPQPL 326
QY 187 LLLLLPVGILLAAWCLHWORTRRTPRP 217
DB 327 -----RAKRPRP 333

RESULT 17
US-10-155-881-7333
Sequence 7333, Application US/10155881
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Lufiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS

FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 7333
LENGTH: 834
TYPE: PRT
ORGANISM: zea mays
US-10-155-881-7333

Query Match 7.1%; Score 88.5; DB 6; Length 834;
Best Local Similarity 29.7%; Pred. No. 33;
Matches 27; Conservative 6; Mismatches 23; Indels 35; Gaps 3;

QY 131 LQETSOVALKPMITRONFSRCLQCOQPDSTLP---PMSPPLEATAPTAQPPL 186
DB 496 LPMSSSLMADSDW-----RSLKVQWDEPSSILRPDRISFWEVEPLDANPQSPQPL 548
QY 187 LLLLLPVGILLAAWCLHWORTRRTPRP 217
DB 549 -----RAKRPRP 555

RESULT 18
US-10-109-324-2
Sequence 2, Application US/10109324
GENERAL INFORMATION:
APPLICANT: Hinayana L. Bawagan
APPLICANT: Kathryn B. Freeman
APPLICANT: Xiatong Li
TITLE OF INVENTION: Polynucleotide and Polypeptide Sequence
FILE REFERENCE: GP50045
CURRENT APPLICATION NUMBER: US/10/109,324
CURRENT FILING DATE: 2002-03-28
PRIORITY APPLICATION NUMBER: 60/280,397
PRIORITY FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1257
TYPE: PRT
ORGANISM: human
US-10-109-324-2

Query Match 7.1%; Score 88.5; DB 6; Length 1257;
Best Local Similarity 23.1%; Pred. No. 54;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

QY 21 SSGISGTQDCSFQHSPISSDFAVKIRLSLDYLDYPTVAVSNLODELC---GGLMRL 76
DB 975 SAGASGSKDAVPCGP-----GVLSDRLCLA--LDEPOLNGHMGASRR 1019
QY 77 VLAQRMRERLKTAVAGSKMOGLLERVNTIEHVTCAFQPPPCSLRFQTNISRLLOETSE 136
DB 1020 VESGAMAYLSPVLARKLESIVENEGSEV-----LALPELPSAHPRIIFMLLWTFQRL-- 1072
QY 137 QLVALKPMITRONFSRCLQCO--PDSSTLPVPW--SPRPLEA-----TAPTAQPP 185
DB 1073 RLPSITPELVAS-----CDGPPSHSQAPSPWLTPDPASVQVRLMDVLTDPDPSGCP 1124
QY 186 LLLLLPVGILLAAWCLHWORTRRTPRPQGVPPVSPQDILLVE 234
DB 1125 LYL-----WRVHSQ--IPQRVWPG---PVASISLALLE 1155

RESULT 19
US-10-174-363-30
Sequence 30, Application US/10174363
GENERAL INFORMATION:
APPLICANT: Butler, Karlene H.

PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 479
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-108-605-57

Query Match 7.0%; Score 87.5; DB 6; Length 479;
Best Local Similarity 22.9%; Pred. No. 20;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MTVALPAMSPPTLL--LLISSGLSTGDCSFQHSPISSDPAVKIRELSDYLLDYP 57
DB 72 MGLISPGSGFQRIYRQKRIIPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
QY 58 VTVAANIQDELCGGLMRLVLAQRMERLKTIVAGSKMGGLLERVNTIEHFVTKCAFQPPP 117
DB 118 CSMESSMDDE-----YMELEFEMESQO-----QTALGF-----P 146
QY 118 SCLFVQTNISRLQETSEQVALKP---WTRONFSRCLQ-OCOPDSSLPPMSPRP 173
DB 147 SGLN-----SLISQIKQPAKSPAGISMRRPSVRCLSMTEBNTNSTTTPPKTPE- 199
QY 174 LEATAPA---PPPLLILLPLVGLLLAAWCLHMORTRRPRPGEQVPVPSPDL 230
DB 200 --TARDCFRPPEP-----ASANCSPISQSKRRHCATVEKENCAPASPLSQ 242
QY 231 LLYEH 235
DB 243 VTISH 247

RESULT 23
PCT-US02-17598-104
Sequence 104, Application PC/TUS0217598
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea N.
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.42012PC
CURRENT APPLICATION NUMBER: PCT/US02/17598
CURRENT FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 570
TYPE: PRT
ORGANISM: Leishmania major
PCT-US02-17598-104

Query Match 7.0%; Score 87.5; DB 1; Length 570;
Best Local Similarity 26.7%; Pred. No. 25;
Matches 48; Conservative 26; Mismatches 63; Indels 43; Gaps 10;

QY 4 LAPWSPPTLL--LLISSGLSTGDCSFQHSPISSDPAVKIRELSDYLLDYP--- 59
DB 174 LPPWSSMPNINAVELKRLKLSGT-----LPADWS-SLKSLSNVLEDTPTGILLP 223
QY 60 --VASNIQDELCGGLMRLV--LAQRW--MERLK--TVAGSKMGGLLERVNTIEHFVTKC 111

DB 224 PNASLERIQDLVRLKRLTGLPIPPWSSMKTIQVLITDGRVSGTL----- 270
QY 112 AFOPPSCLEFVQTNISRLQETSEQVALKP-WTRONFSRCLQ-OCOPDSSLPPMSPRP 170
DB 271 ---PPWSSAMASVRIILNT--EGTEVSGTLPPWSSMKTL-OTLNLRTKVSGLTLPPEWS 323

RESULT 24
US-10-032-214-174

Sequence 174, Application US/10032214

GENERAL INFORMATION:
APPLICANT: PUNNONEN, JUHA
APPLICANT: LAZETIC, ALEXANDRA
APPLICANT: LEONG, STEVEN R.
APPLICANT: CHANG, CHIA-CHUN
APPLICANT: APT, DORIS
APPLICANT: GUSTAFSSON, CLAES
TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
FILE REFERENCE: 02-106730US
CURRENT APPLICATION NUMBER: US/10/032,214
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/888,324
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: PCT/US01/19973
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/241,245
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 174
LENGTH: 303
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (75)
OTHER INFORMATION: Variable amino acid
US-10-032-214-174

Query Match 7.0%; Score 87; DB 6; Length 303;
Best Local Similarity 24.0%; Pred. No. 13;
Matches 58; Conservative 36; Mismatches 66; Indels 82; Gaps 18;

QY 15 LLLISSGLSTGDCSFQHSPISSDPAVKIRELSDYLLQ---DYPTVASNLQDEE--- 68
DB 103 IYIALLRISDSGTYCTVQKPKDG--AVKLEHLTSVRLMIRADPPVPTINDLNPSPNI 160
QY 69 ---LC---GGLMRLVLAQRMERLKTIVAGSKMGGLLERN---TEHFVTKCAFQPPPS 118
DB 161 RRLICSTSGFPRPHT--YMLEN-----GELNATNTVSDQPGELTMIS-----S 205
QY 119 CLRFVQTNISRLQETSEQVALKP---WTRONFSRCLQ-OCOPDSSLPPMSPRP 175
DB 206 ELDFNVIN-----NHSIVCLIKYGELLVSGIF-----PMS-KPKQ 239
QY 176 ATAPAPQPPILLI---LLIPV-GLLILAA--WCL-----HMORTRRTPRG-ECVP 222
DB 240 -----EPPIQQLPFVWIIIPVSGALVLAIVLYYCLACHRAVRMRKRRNEETVGTERTS 292
QY 223 PV 224
DB 293 PI 294

RESULT 25
US-10-032-214-177

```
; Sequence 177, Application US/10032214
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-10673005
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 177
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-032-214-117
```

```
Query Match 7.0%; Score 87; DB 6; Length 303;
Best Local Similarity 24.4%; Pred. No. 13;
Matches 59; Conservative 34; Mismatches 67; Indels 82; Gaps 18;

QY 15 LLLLLSSGLSTGQDCSPQSPSSDFAVKIRELSYLIQ---DYPVTVASNLQDEE--- 68
Db 103 IYILALSLSDSGTYTCVIOKPVKKG--AYKLEHLASVRLMIRADFPVPTINDGNPSPNI 160
QY 69 ---LC--GGLMRLVLAQRMERLKTAGSKMOGLLERN---TEIHFTKCAFQPPPS 118
Db 161 RRLICSTSGGFPBPRL--WLEN---GSELNATWTYVSODPGTELYMIS-----S 205
QY 119 CLRFVQTNISRLQETSEQVYALKPW---ITQNFESRCLELQCPDSDSTLPPMSRPPL 175
Db 206 ELDPNVTN-----NHSIVCLIKIGELSVSOLF-----PWS-KPKQ 239
QY 176 ATAFTAPQP--LLLLLPV-GLDLAA--WCL-----HMQTRRRRTPRG-EQVP 222
Db 240 -----EPPIQLPFLVITPVSGALVLTAVVLYCLACRHRVAMWKTRRNETVGTERTLS 292
QY 223 PV 224
Db 293 PT 294
```

Search completed: August 6, 2002, 09:41:14
Job time: 225 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:34:49 ; Search time 22.73 Seconds
(Without alignments)
252,530 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MVLAPAWSPPTLYLLLL.....RPGQVPPVSPQDLLEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCNUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 US-08-243-545-6	Sequence 6, Appl1
2	1242	100.0	235	2 US-08-993-962-6	Sequence 6, Appl1
3	1242	100.0	235	4 US-09-160-841-6	Sequence 6, Appl1
4	1242	100.0	235	4 US-09-109-100-1	Sequence 1, Appl1
5	1242	100.0	235	5 PCT-US94-05365-6	Sequence 6, Appl1
6	1124	90.5	212	4 US-09-109-100-10	Sequence 10, Appl1
7	1114	89.7	209	4 US-09-109-100-18	Sequence 18, Appl1
8	1110	89.4	209	4 US-09-109-100-9	Sequence 9, Appl1
9	1110	89.4	209	4 US-09-109-100-12	Sequence 12, Appl1
10	1110	89.4	209	4 US-09-109-100-14	Sequence 14, Appl1
11	1110	89.4	209	4 US-09-109-100-17	Sequence 17, Appl1
12	1108	89.2	209	4 US-09-109-100-11	Sequence 11, Appl1
13	1108	89.2	209	4 US-09-109-100-15	Sequence 15, Appl1
14	1107	89.1	209	4 US-09-109-100-13	Sequence 13, Appl1
15	1106	88.0	209	4 US-09-109-100-8	Sequence 8, Appl1
16	1100	88.6	209	4 US-09-109-100-16	Sequence 16, Appl1
17	768.5	61.9	231	1 US-08-243-545-2	Sequence 2, Appl1
18	768.5	61.9	231	2 US-08-993-962-2	Sequence 2, Appl1
19	768.5	61.9	231	4 US-09-160-841-2	Sequence 2, Appl1
20	768.5	61.9	231	5 PCT-US94-05365-2	Sequence 2, Appl1
21	765.5	61.6	231	1 US-08-220-3798-7	Sequence 7, Appl1
22	765.5	61.6	231	5 PCT-US95-03866-6	Sequence 6, Appl1
23	506.5	40.8	137	4 US-09-109-100-1	Sequence 19, Appl1
24	154	12.4	42	5 PCT-US94-05150-17	Sequence 17, Appl1
25	91.5	7.4	675	1 US-08-317-522A-9	Sequence 9, Appl1
26	91.5	7.4	675	1 US-08-439-818A-9	Sequence 9, Appl1
27	91.5	7.4	675	2 US-08-751-965-9	Sequence 9, Appl1

28	91.5	7.4	675	2 US-08-738-975-9	Sequence 9, Appl1
29	91.5	7.4	675	2 US-08-728-626-9	Sequence 9, Appl1
30	91.5	7.4	675	3 US-08-808-599A-9	Sequence 9, Appl1
31	87.5	7.0	415	4 US-09-006-353A-6	Sequence 8, Appl1
32	85	6.8	366	1 US-08-004-492-8	Sequence 4, Appl1
33	84.5	6.8	913	1 US-08-445-640-4	Sequence 4, Appl1
34	84.5	6.8	913	3 US-08-170-558-4	Sequence 4, Appl1
35	84.5	6.8	913	3 US-08-447-314-4	Sequence 4, Appl1
36	84.5	6.8	913	3 US-08-445-461-4	Sequence 4, Appl1
37	84	6.8	107	4 US-09-220-528-52	Sequence 52, Appl1
38	84	6.8	220	4 US-09-220-528-26	Sequence 26, Appl1
39	83.5	6.7	429	1 US-07-964-589-2	Sequence 2, Appl1
40	83.5	6.7	429	5 PCT-US93-02024-2	Sequence 2, Appl1
41	83.5	6.7	671	3 US-09-121-321-16	Sequence 16, Appl1
42	83.5	6.7	671	4 US-08-933-803A-16	Sequence 16, Appl1
43	83	6.7	726	5 PCT-US94-05150-12	Sequence 12, Appl1
44	83	6.7	738	1 US-07-756-250-16	Sequence 16, Appl1
45	82.5	6.6	249	2 US-08-632-514C-11	Sequence 11, Appl1
46	82.5	6.6	249	3 US-09-188-177-11	Sequence 11, Appl1
47	82.5	6.6	513	2 US-08-357-533A-11	Sequence 11, Appl1
48	82.5	6.6	513	2 US-08-459-009-11	Sequence 11, Appl1
49	82.5	6.6	513	3 US-08-459-951-11	Sequence 11, Appl1
50	82.5	6.6	528	4 US-08-928-213B-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for fli3/fliK-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
DB 1 MTVLAPAMSPPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
QY 61 ASNLODEELCGLMRLVLAQRMMERLKTVAAGSKMOGLLERVNTETHEFTKCAFPQPPSCL 120
DB 61 ASNLODEELCGLMRLVLAQRMMERLKTVAAGSKMOGLLERVNTETHEFTKCAFPQPPSCL 120
QY 121 RFOVNTISRLQETSEQVLAKFWITRONFSRCLELOCOPDSSSTLPPMSRPLEATAPT 180
DB 121 RFOVNTISRLQETSEQVLAKFWITRONFSRCLELOCOPDSSSTLPPMSRPLEATAPT 180
QY 181 APOPELLLLLLPVGILLAAACLMHOMTRRRTRPRGEOVPVPSPDOLLVEH 235
DB 181 APOPELLLLLLPVGILLAAACLMHOMTRRRTRPRGEOVPVPSPDOLLVEH 235

RESULT 2
US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
DB 1 MTVLAPAMSPPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
QY 61 ASNLODEELCGLMRLVLAQRMMERLKTVAAGSKMOGLLERVNTETHEFTKCAFPQPPSCL 120
DB 61 ASNLODEELCGLMRLVLAQRMMERLKTVAAGSKMOGLLERVNTETHEFTKCAFPQPPSCL 120
QY 121 RFOVNTISRLQETSEQVLAKFWITRONFSRCLELOCOPDSSSTLPPMSRPLEATAPT 180
DB 121 RFOVNTISRLQETSEQVLAKFWITRONFSRCLELOCOPDSSSTLPPMSRPLEATAPT 180
QY 181 APOPELLLLLLPVGILLAAACLMHOMTRRRTRPRGEOVPVPSPDOLLVEH 235
DB 181 APOPELLLLLLPVGILLAAACLMHOMTRRRTRPRGEOVPVPSPDOLLVEH 235

RESULT 3
US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:

[illegible]

PCT-US94-05365-6

Query Match	100.0%;	Score 1242;	DB 5;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 1.6e-117;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0;

```
QY 1 MTVLAPAMSPPTYLLLLLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDPYV 60
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 1 MTVLAPAMSPPTYLLLLLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDPYV 60
QY 61 ASNIODEELCGGLMRLVLAQRMERLKTAVAGSKMGLERVNTIEHFVTKCAFQPPPSCL 120
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 61 ASNIODEELCGGLMRLVLAQRMERLKTAVAGSKMGLERVNTIEHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLQCCPDSSSTLPWPSPPLEATAPT 180
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLQCCPDSSSTLPWPSPPLEATAPT 180
QY 181 APOPRLILLLPVGILLAAAWCLHMORTRRTPRPGQVPPVPSQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 181 APOPRLILLLPVGILLAAAWCLHMORTRRTPRPGQVPPVPSQDILLVEH 235

RESULT 6
US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

Query Match 90.5%; Score 1124; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.1e-105;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGQDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNIODEELCGGLMRLVLAQRM 84
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 2 SGQDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNIODEELCGGLMRLVLAQRM 61
QY 85 RLKTAVAGSKMGLERVNTIEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPW 144
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 62 RLKTAVAGSKMGLERVNTIEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPW 121
QY 145 ITRQNSRCLQCCPDSSSTLPWPSPPLEATAPTAPQPPILLLLPVGLLLAAAWC 204
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 122 ITRQNSRCLQCCPDSSSTLPWPSPPLEATAPTAPQPPILLLLPVGLLLAAAWC 181
QY 205 LHMORTRRTPRPGQVPPVPSQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 182 LHMORTRRTPRPGQVPPVPSQDILLVEH 212

RESULT 7
US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
```

```
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

Query Match 89.7%; Score 1114; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNIODEELCGGLMRLVLAQRMERL 86
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNIODEELCGGLMRLVLAQRMERL 60
QY 87 KTVAGSKMGLERVNTIEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWIT 146
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 61 KTVAGSKMGLERVNTIEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNSRCLQCCPDSSSTLPWPSPPLEATAPTAPQPPILLLLPVGLLLAAAWCLH 206
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 121 RQNSRCLQCCPDSSSTLPWPSPPLEATAPTAPQPPILLLLPVGLLLAAAWCLH 180
QY 207 WQTRRRTPRPGQVPPVPSQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 181 WQTRRRTPRPGQVPPVPSQDILLVEH 209

RESULT 9
US-09-109-100-12
; Sequence 12, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
```

APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 12
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-12

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.7e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 60
QY 87 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 146
DB 61 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 120
QY 147 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 206
DB 121 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 180
QY 207 WQTRRRTPRPGEOVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRPGEOVPPVPSQDILLVEH 209

RESULT 10
US-09-109-100-14
Sequence 14, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 14
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.7e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 60
QY 87 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 146
DB 61 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 120
QY 147 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 206
DB 121 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 180
QY 207 WQTRRRTPRPGEOVPPVPSQDILLVEH 235

DB 181 WQTRRRTPRPGEOVPPVPSQDILLVEH 209

RESULT 11
US-09-109-100-17
Sequence 17, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 17
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.7e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 60
QY 87 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 146
DB 61 KTVAGSKMGLERVTETHEFTKCAFOPPPSCLEFVQTNISRLQETSEQVALKPMT 120
QY 147 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 206
DB 121 RQNSRCLLEQCCPDSSITLPPMSRPLEATAPAPQPLLILLPVGILLAAACGLH 180
QY 207 WQTRRRTPRPGEOVPPVPSQDILLVEH 235
DB 181 WQTRRRTPRPGEOVPPVPSQDILLVEH 209

RESULT 12
US-09-109-100-11
Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.3e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLODEELCGLMRLVLAORMMERL 60

```
OY      87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120
OY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
OY      207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209
```

```
RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-109-100-15
```

```
Query Match      89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
OY      87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120
OY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
OY      207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209
```

```
RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-109-100-13
```

```
Query Match      89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 5.4e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
OY      87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120
OY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
OY      207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209
```

```
RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-109-100-8
```

```
Query Match      89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
OY      87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLQETSEQVALKPWIT 120
OY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
OY      207 WQTRRRTRPRGEQVPPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEQVPPVPSPODLLVEH 209
```

```
RESULT 16
US-09-109-100-16
; Sequence 16, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
```

```

: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 16
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-109-100-16

```

```

Query Match      88.6%; Score 1100; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2,7e-103;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 27 TQDGFHSPISDFPAVKIRELSYLLQDYPVIVASNLQDEELGGIMRLVLAQRMERL 86
Db 1 TQDGFHSPISDFPAVKIRELSYLLQDYPVIVASNLQDEELGGIMRLVLAQRMERL 60
QY 87 KTVAGSKMGLLEVRNTEIHVTKCAFPQPPSCLEFVQTNISRLQETSQLVALKPMIT 146
Db 61 KTVAGSKMGLLEVRNTEIHVTKCAFPQPPSCLEFVQTNISRLQETSQLVALKPMIT 120
QY 147 RQNSRCLQLQCPDSSSTLPPWSPRELEATAPAPQPLLLLLPVGLLLAAACMLH 206
Db 121 RQNSRCLQLQCPDSSSTLPPWSPRELEATAPAPQPLLLLLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRRGEQVPVPPSPQDLLVEH 235
Db 181 WQTRRRTPRRGEQVPVPPSPQDLLVEH 209

```

```

RESULT 17
US-08-243-545-2
: Sequence 2, Application US/08243545
: Patent No. 5534512
: GENERAL INFORMATION:

```

```

: APPLICANT: Lyman, Stewart D.
: APPLICANT: Beckmann, M. Patricia
: TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 7.0.1
: SOFTWARE: Microsoft Word, Version #5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/243,545
: FILING DATE: 11-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/162,407
: FILING DATE: 03-DEC-1993
: APPLICATION NUMBER: 08/111,758
: FILING DATE: August 25, 1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/106,463
: FILING DATE: August 12, 1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/068,394
: FILING DATE: May 24, 1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Malaska, Stephen L.
: APPLICATION NUMBER: 32,655
: FILING DATE: May 24, 1993

```

```

: REFERENCE/DOCKET NUMBER: 2813-C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEEX: 756822
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 231 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-243-545-2

```

```

Query Match      61.9%; Score 768.5; DB 1; Length 231;
Best Local Similarity 70.3%; Pred. No. 8e-70;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
QY 1 MVLAPAWSP-TTYLLILLSSGSGTQDCSFQHSPISSDFPAVKIRELSYLLQDYPVT 59
Db 1 MVLAPAWSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
QY 60 VASNLQDEELGGIMRLVLAQRMERLKTIVAGSKMGLLEVRNTEIHVTKCAFPQPPSC 119
Db 61 VAVNLQDEELGGIMRLVLAQRMERLKTIVAGSKMGLLEVRNTEIHVTKCAFPQPPSC 120
QY 120 LRFVQTNISRLQETSQLVALKPMITR--QNSRCLQLQCPDSSSTLPPWSPRELEAT 177
Db 121 LRFVQTNISRLQETSQLVALKPMITR--QNSRCLQLQCPDSSSTLPPWSPRELEAT 180
QY 178 APTAPQP--LLILLLLPVGLLLAAACMLHQRTRRRTPRRGEQVPVPPSP 227
Db 181 ELPEPRQQLLLILLLLPVGLLLAAACMLHQRTRRRTPRRGEQVPVPPSP 228

```

```

RESULT 18
US-08-993-962-2
: Sequence 2, Application US/08993962
: Patent No. 5843423
: GENERAL INFORMATION:
: APPLICANT: Lyman, Stewart D.
: APPLICANT: Beckmann, M. Patricia
: TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 7.0.1
: SOFTWARE: Microsoft Word, Version #5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/993,962
: FILING DATE: December 18, 1997
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/162,407
: FILING DATE: December 3, 1993
: APPLICATION NUMBER: 08/111,758
: FILING DATE: August 25, 1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/106,463
: FILING DATE: August 12, 1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/068,394
: FILING DATE: May 24, 1993

```


PCT-US95-03866-6

best local similarity 69.8%; Pred. NO. 1.0e-69;
Matches 162; Conservative 18; Mismatches 43; Indels 9; Gaps 4

Db 181 ELPEPRRQLLLLLLPLTLVLAAWGLRWQRARRK ---GELHPGVLP 228

US-09-109-100-19

Matches 101; Conservative 11; Mismatches 22; Indels 3; Gaps 2;

Db 121 GKACQNF SRCLEVQCCP 137

PCT-US94-05150-17

; GENERAL INFORMATION:

APPLICANT:

TITLE OF I

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk

```

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 5.1a

```
; CURRENT APPLICATION DATA:
```

FILING DATE:

; PRIOR APPLICATION DATA:

FILING DATE: 03-DEC-1993

; PRIOR APPLICATION DATA:

ACCESSION NUMBER: 05 08/199/111
 FILING DATE: 19-NOV-1993

;
PRIOR APPLICATION DATA:

FILED DATE: 24-AUG-1993

;
PRIOR APPLICATION DATA:

AFFILIATION NUMBER: US 08/100,340
 FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/092,349

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,263

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/065,231

ELIING DATE: 13 MAY 1953

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids
TYPE: amino acid

```
! TOPOLOGY: linear
```

MOLECULE TYPE: peptide
DCM-HC04-0E1E0-17

Query Match	Score	DB	Length
12.48;	154;	DB 5;	Length 42;

Matches	30;	Conservative	5;	Mismatches	7;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

[illegible]

Db 1 TPDGYFHSPISSNEKVKFRELTVHLLKDYPTVAVNLÖDEK 42

RESULT 25

US-08-31/-522A-9

Patent No. 5599918


```

1  GENERAL INFORMATION:
2  APPLICANT: Fukuda, Michiko N.
3  TITLE OF INVENTION: Trophobin and Trophobin-Assisting
4  TITLE OF INVENTION: Proteins
5  NUMBER OF INVENTION: Proteins
6  NUMBER OF SEQUENCES: 13
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Campbell and Flores
9  STREET: 4370 La Jolla Village Drive, Suite 700
10 City: San Diego
11 STATE: California
12 COUNTRY: USA
13 ZIP: 92122
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patentin Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/317,522A
22 FILING DATE: 04-OCT-1994
23 CLASSIFICATION: 536
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Campbell, Cathryn A.
27 REGISTRATION NUMBER: 31,815
28 REFERENCE/DOCKET NUMBER: P-LA 9991
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (619) 535-9001
31 TELEFAX: (619) 535-8949
32 INFORMATION FOR SEQ ID NO: 9:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 675 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38
39 US-08-317-522A-9

```

```

Query Match 7.4% Score 91.5; DB 1; Length 675;
Best Local Similarity 27.7% Pred. No. 0.57;
Matches 31; Conservative 13; Mismatches 29; Indels 39; Gaps 4

QY 111 CAGPPSCIRFQVIMISRLQETSEQVALKPMTTRNESCSELCQCPDSSITPPWS 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 CSRDPISC-----VPLPSLRSLRRSLRPLPRKGPRIHPQLVYVK-----KPF 46
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 171 PRPLEATAPTAPOPILLILLIPVGLILLIAAWCLHWORTRRRTPRGEOYP 222
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 PTP-----PTTRKPPPLPKLL-----RKTPDESPVP 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
Search completed: August 6, 2002, 09:39:37
Job time: 288 sec
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:40:23 ; Search time 32.24 Seconds

(without alignments)
688.481 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MTVLAPAMSPNSLLLLLLL.....WQARRRGELHPGVLPDPSHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

1: PIR.71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1223	100.0	231	2	A49265	flt3/flk-2 ligand
2	879	71.9	220	2	S43291	FLT3/FLK2 ligand (
3	879	71.9	220	2	I58343	flt3 ligand isofor
4	768.5	62.8	235	2	I38440	flt3 ligand - huma
5	616.5	50.4	245	2	S43293	FLT3/FLK2 ligand (
6	594.5	48.6	178	2	I39076	flt3 ligand altern
7	95.5	7.8	909	1	A54809	disease resistance
8	88	7.2	843	2	T01438	hypothetical prote
9	87	7.1	291	2	AF0123	probable antigenic
10	86	7.0	962	2	C71617	SERA antigen/papa
11	85	7.0	181	2	T20323	hypothetical prote
12	84.5	6.9	939	2	E82121	peptidase, insulin
13	84	6.9	1409	2	T37188	presynaptic activi
14	83.5	6.8	552	1	A31401	macrophage colony
15	83.5	6.8	552	1	S35703	colony-stimulating
16	83.5	6.8	2476	2	T34022	zonahesin - pig
17	82.5	6.7	378	2	S00842	leukostatin precur
18	82.5	6.7	431	2	T04868	hypothetical prote
19	81	6.6	4131	2	T21085	hypothetical prote
20	80.5	6.6	391	2	B40892	apolipoprotein A-I
21	80.5	6.6	394	2	A25281	apolipoprotein A-I
22	80.5	6.6	395	2	A40892	apolipoprotein A-I
23	80	6.5	382	2	E84527	hypothetical prote
24	79.5	6.5	399	2	C40892	apolipoprotein A-I
25	79.5	6.5	745	2	T38299	probable beta-adap
26	79	6.5	1101	2	S58108	hypothetical prote
27	78.5	6.4	122	2	D70730	hypothetical prote
28	78.5	6.4	315	2	T24821	hypothetical prote
29	78.5	6.4	379	2	T11349	ubiquinol-cytochr

30	78.5	6.4	468	2	T23091	hypothetical prote
31	78.5	6.4	3068	1	A44062	genome polyprotein
32	78	6.4	224	2	I37243	CMR-35 antigen
33	78	6.4	743	2	T34632	probable bi-functi
34	78	6.4	806	2	E64221	phenylalanine--trn
35	78	6.4	908	2	S51293	probable membrane
36	78	6.4	1601	2	AE2011	hypothetical prote
37	78	6.4	1715	2	T06145	disease resistance
38	77.5	6.3	266	2	A45844	MHC class II histo
39	77.5	6.3	456	2	B72130	frame-shift with c
40	77.5	6.3	579	2	JC7629	membrane-type friz
41	77.5	6.3	746	2	S67203	probable membrane
42	77.5	6.3	774	2	B86492	hypothetical prote
43	77.5	6.3	774	2	H81540	hypothetical prote
44	77.5	6.3	811	2	E72003	hypothetical prote
45	77	6.3	619	2	D86509	S/T protein kinase
46	77	6.3	619	2	A72114	sodium/phosphate c
47	77	6.3	653	2	A54366	hypothetical prote
48	77	6.3	1509	2	T19486	conserved hypothet
49	76.5	6.3	222	2	D69026	glycoprotein VP7 p
50	76.5	6.3	326	1	VGXR1S	

ALIGNMENTS

RESULT 1
A49265
flt3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence,revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Hoall
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791
A:Accession: A49265
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYM>
A:Cross-references: GB:I23636; NID:9439441; PIDN:AAA9436.1; PID:9439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I49347
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'V', 198-231 <RE2>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zuzawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelnier, G.; Namiakawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 366, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi
A:Reference number: S43290; MUID:94195428
A:Accession: S43290
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'V', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Genetics: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein

Query Match 100.0%; Score 1223; DB 2; Length 231;

Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
Db 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
QY 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
Db 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
Db 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
QY 181 ELPRPRRQQLLLLLPLTVLLAAAGLRMQRARRRGLHPGVPLPSHP 231
Db 181 ELPRPRRQQLLLLLPLTVLLAAAGLRMQRARRRGLHPGVPLPSHP 231

```

RESULT 2

FLT3/FLK2 ligand (clone T118) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43291
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka-
felt, A.; Muench, M.; Keilner, G.; Nankikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43291
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <HAN>

Query Match 71.9%; Score 879; DB 2; Length 220;
Best Local Similarity 82.3%; Pred. No. 1e-70; Indels 12; Gaps 3;

```

QY 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
Db 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
QY 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
Db 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
Db 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
QY 177 LEATELPEPRRQQLLL-----LLLLPLTVLLAA 206
Db 178 LTATALLTVCPLLPLVGTSHMFPLPYELSLSS 212

```

RESULT 3

flt3 ligand isoform 5H - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58343
R:Llyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K.
Oncogene 10, 149-157, 1995
A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand
A:Reference number: I58343; MUID:95124210
A:Accession: I58343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-220 <RES>
A:Cross-references: GB:S76459; NID:99134479; PIDN:AA33069.1; PID:9913480

Query Match 71.9%; Score 879; DB 2; Length 220;
Best Local Similarity 82.3%; Pred. No. 1e-70;
Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

```

QY 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
Db 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
QY 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
Db 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
Db 121 LRFVQTNISHLKDTCTQLLALKPCIGKACQNSRCLEVOCCOPDSSSTLLPRSPALAEAT 180
QY 177 LEATELPEPRRQQLLL-----LLLLPLTVLLAA 206
Db 178 LTATALLTVCPLLPLVGTSHMFPLPYELSLSS 212

```

RESULT 4

flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Llyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842
A:Accession: I38440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U02874; NID:9494978; PIDN:AAA19825.1; PID:9494979
R:Llyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U02874; NID:91072036; PIDN:AAA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka-
felt, A.; Muench, M.; Keilner, G.; Nankikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', 73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
A:Note: the authors translated the codon AGR for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 62.8%; Score 768.5; DB 2; Length 235;
Best Local Similarity 70.3%; Pred. No. 7.1e-61;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

```

QY 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
Db 1 MTVALPAMSPNSLLILLILSLPCLRGTPDCYFSHPISSNFKVKFRELTDHLKDPVT 60
QY 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120
Db 61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTETIHFTVSCFOPLPPEC 120

```


QY 149 ACQNFSCLEVOCCPDSSTLLPPRSPIALTEATEPEPRROLTLTLPLTVLLAAW 208
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 715 HGRNRR-LSIKSCHDELIV---TPADFENDMLPS--LEVLTLHSLHNLTRV-----W 762
 QY 209 G 209
 Db 763 G 763

RESULT 8
 T01438
 hypothetical protein GS034D21.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Nov-1999
 C:Accession: T01438
 R:Smith, A.; Harmon, G.; Elliott, G.; Tryman, B.
 Submitted to the EMBL Data Library, November 1997
 A:Description: The sequence of H. sapiens BAC clone GS034D21.
 A:Reference number: Z14332
 A:Accession: T01438
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-843 <SMI>
 A:Cross-references: EMBL:AC003077; NID:g2588634; PIDN:AAE83946.1; PID:g2588635
 C:Genetics:
 A:Map position: 7
 A:Note: Intron positions not resolved (incomplete sequence)
 A:Note: WUGSC:H_GS034D21.1

Query Match 7.28; Score 88; DB 2; Length 843;
 Best Local Similarity 20.18; Pred. No. 8.7;
 Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
 QY 27 GTPCCYFHSHPISSNFYKFRRLDHLK--DYPVTVAVNLDEKCKALW----SLFL 79
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 483 GVPD-----NIKSFYK-----NHMKRYDRPFHKGR-DKENEFKSLWERTSLYL 529
 QY 80 AQ-----RW-IEQLTVAGSKMQT--LLEDVTEIH-FVTSQ-----TFQPLPECL 121
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 530 VQSLPGISRWFEVKEKREVENSPLENAIEVLKNNQOLKTLISQCCQROMQNNPLMCL 569
 QY 122 -----RYV 124
 Db 590 NGVIDAAVNGVSNRYQDAFVKEYIILSHPEDGKIARLEMLEQAQILFGLAVHEKRV 649
 QY 125 QTNISHLKDTCTQLALKPCIGKACQNSRCLEVO-----CQ-----PDS 165
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 650 PQDMRPLHKKLIVQDFEYFKSSLG--IQEFSACMQASVYHPNPGSPYCRNSAPASVSDG 707
 QY 166 STLLPPRSPIALEA 179
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 708 TRVLRPSRPLSTPA 721

RESULT 9
 AF0123
 probable antigenic leucine-rich repeat protein YP01006 [imported] - Yersinia pestis (str
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AF0123
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deon-Tarraga, A.M.; Chillingworth, T.; Croxin, A.; Davies, R.M.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0123
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89849.1; PID:g15979075; GSPDB:GN00175
 C:Genetics:

A:Gene: YP01006

Query Match 7.18; Score 87; DB 2; Length 291;
 Best Local Similarity 23.88; Pred. No. 3.2;
 Matches 50; Conservative 30; Mismatches 62; Indels 68; Gaps 11;
 QY 56 DYPVTVAVNLDEKCKALMSFLAQRWIEQLKYAG-----SKMOTLEDVTEIHF 108
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 24 DRPAATALTLPAD---YHAIW-----EKWENDPRTVAGEQGAARMKECLEN-NAERLN 74
 QY 109 VNSCTFQPLPE---C--TRFYQTNISHL-----LKDTCTQLALKPCIGKACQN 152
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 75 ISSLDITSLPDLPCNENLITCNNTLPTLTPNLOTLKASYQNLKPLPVPASLIS 134
 QY 153 FS-----RCLEVOCCPDSSTLLPPRSPIALEA-----TELP----- 183
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 135 LKVMNELRLPEPLPEGLKTLDVGC--NTSLQPSRLPPVLESLSISNCLTELPPLN 192
 QY 184 -----EPRROLTLTLPLTVLLAAW 208
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 193 SLKELDAHGNQLRLPDTPLISLRINAV 222

RESULT 10
 C71617
 SERR antigen/papain-like proteinase with active Ser PRB0345C - malaria parasite (Plas
 C:Species: Plasmodium falciparum
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: C71617
 R:Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
 ; Petteh, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
 Science 282, 1126-1137, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A11600; MUID:99021743
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-962 <GAR>
 A:Cross-references: GB:AE001388; GB:AE001362; NID:g3845157; PIDN:AAC71858.1; PID:g384
 A:Experimental source: clone 3D7
 C:Genetics:
 A:Gene: PRB0345C
 A:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 7.04; Score 86; DB 2; Length 962;
 Best Local Similarity 20.98; Pred. No. 15;
 Matches 31; Conservative 28; Mismatches 39; Indels 50; Gaps 7;
 QY 8 WSPNSLLLLLLSPCLRGTPDCYFSSHPSISNF-----KYKFRRLDHL----- 53
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 422 WMKNKTGTLV-----PQLSYDLTYKNNFTFTQKSTQSNIVDKLCHNEYC 470
 QY 54 --LKDPVTVA-VNLDEKCKALMSFLAQRWIEQLKYAGSKMQTLLEDVTEIHFVT 110
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 471 NKLKHNNCKISKINVEDKNCALSWA-FASKYHLETIKCMKG-----YELNASVLYVT 523
 QY 111 SCTFQPLPECLRFVQTNISHLKDTCTQ 138
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 524 NC-----LKNKNKDYCTE 536

RESULT 11
 T20323
 hypothetical protein D1086.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20323
 R:Smeye, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19257
 A:Accession: T20323


```

Db 59 ARASSIPPL-----CTPLSSFFFTSAGASGNTVP--ELTTSGEVSSTEASLVLP 106
QY 51 --DHLKDPYTVAVNLODEKHKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHF 108
Db 107 KSSGASDPVPVIT-----NPATSSAVASTLEFETKGSAPPV-----145
QY 109 VNSCFEQLPECLRVQTNIS-----HLKDTCTOLLALKPCIG 147
Db 146 VTSSTMTSGP---FVATVTSSTSGPPVMTATGSLGPSKETHGLSATIATSSGESSVA 201
QY 148 KACONFSRCLEVOCCPDSSTLLPSPRIALTELEPEPRPOLLLLLLPVLVLA 207
Db 202 GGTPEVSTKISTSTSPNNTTTPPR-----PGSSGMILVSLMLIVLVLA 249
QY 208 WGLRM-QQARRR 218
Db 250 LLLMROROKRR 261

```

```

RESULT 18
T04868
hypothetical protein F28A21.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04868
R:Bayan, M.; Mueller, M.W.; Muehle, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15387
A:Accession: T04868
A:Molecule type: DNA
A:Residues: 1-431 <BEV>
A:Cross-references: EMBL:AI035526
C:Experimental source: cultivar Columbia, BAC clone F28A21
C:Genetics:
A:Map position: 4
A:Note: F28A21.170

```

```

Query Match
Best Local Similarity 6.7%; Score 82.5; DB 2; Length 431;
Matches 49; Conservative 15; Mismatches 63; Indels 55; Gaps 8;

```

```

QY 10 PNSSLLLLLLLS-----PCLRGTPDCYFS---HSPISNFKKRELTHLKLKPYV 59
Db 4 PSLPLLLLLLSATISAASLSPTSPPIPKPSSSSFL-----48
QY 60 TVAVNLODEKHKALMSLFL--AQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPL 117
Db 49 -----DPRQLKALLESINIPYKDCPNHRPTTKSTSSVVTCDTSSPRLVMSISF---98
QY 118 PECLRFVQTNISHLKDTCTOLLALKPCIGKACONFSRCLEVOCCPDSSTLLPSPRIAL 177
Db 99 -----TNCSTDLISISTALRLSPSL--TSLSLFNC-----PSLSP--PPRLPDSL 140
QY 178 EA 179
Db 141 HS 142

```

```

RESULT 19
T21085
hypothetical protein F18C12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T21085
R:Harris, B.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19371
A:Accession: T21085
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4131 <WIL>

```

```

A:Cross-references: EMBL:Z75536; PIDN:CAA99830.1; GSPDB:GN00019; CESP:F18C12.1
A:Experimental source: clone F18C12
C:Genetics:
A:Gene: CESP:F18C12.1
A:Map position: 1
A:Introns: 54/3; 112/3; 146/1; 294/1; 381/3; 455/3; 596/3; 716/3; 743/2; 782/3; 820/3
09/3; 2303/3; 2483/1; 2529/1; 2612/3; 2687/1; 2734/3; 2799/3; 2841/3; 2891/2; 2932/3;
C:Superfamily: dynein heavy chain, cytosolic

```

```

Query Match
Best Local Similarity 6.6%; Score 81; DB 2; Length 4131;
Matches 51; Conservative 28; Mismatches 68; Indels 92; Gaps 11;

```

```

QY 47 RELTHLKDYPYTVAVNLODE-----KHKALMSLFLAQRWIEOLKTVAGSKMOTLL 99
Db 381 QEYIGHSKSVPSV-----DEPTLGLPENIKYSQIYVADRTTSSITLALGDTKNAL 3864
QY 100 EDVNTIEHFVTS-----CTFOPLPE-----CLRFVQT-----NI 128
Db 3865 SDQSDKISQIVSLMKKLCQSDLDLPKRELPTAIRSADPISSEVLCLETINMLSLIKQLHRSI 3924
QY 129 SHLKDTCQLLALKPCIGKACONFSRCLEVOCCP-----164
Db 3925 GHVAKSKMTPSLA-SPAVQRTQS---LVFOQTPEWDSMMAGSPADYLVVYKKTR 3979
QY 165 -----SSTLLPSPRIALTELEPEPR-----PROLLLLLLLPVLVLA 208
Db 3980 GTQLFRESSKSSSL--SSPI--DFSDLYPNFLNALKQTTSRQIKIPLDOLLSSAW 4034

```

```

RESULT 20
B40892
apolipoprotein A-IV precursor - mouse (strain 129)
C:Species: Mus musculus (house mouse)
C:Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C:Accession: B40892
R:Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion
A:Reference number: A40892; MUID:91286309
A:Accession: B40892
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-391 <REU>
A:Cross-references: GB:M64248; NID:g191884; PIDN:AAA37214.1; PID:g191885
C:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 2
C:Superfamily: apolipoprotein A-I
C:Keywords: lipid binding; lipoprotein

```

```

Query Match
Best Local Similarity 6.6%; Score 80.5; DB 2; Length 391;
Matches 37; Conservative 42; Mismatches 69; Indels 27; Gaps 6;

```

```

QY 11 NSSLLLLLLLSPCUR-----GTPDCYFSHPISNFKYK---RELTHL---LK 55
Db 147 NTQTQEMKQLTPYIQRMQTTIKENVNMLHTSMPLATNLKDKFNRMNEELKGLTPRAN 206
QY 56 DYPVTVAVNLODEKHKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFO 115
Db 207 ELKATITDQNLDELRLSLAPLYTGVQEKLNHQWEGIA-FQMKNAEELQTKV---SAKID 261
QY 116 PLPECLRFVQTNISHLKDTCTOLLALKPCIGKACONFSRCLEVOCCPDSSTLLP 170
Db 262 QL-----QKNMLADLVEDVQSKVGNTEGLQKSLHDLNRQLEDOVEEFRTVTP 309

```

```

RESULT 21
A25281
apolipoprotein A-IV precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 13-Aug-1999

```

C:Accession: A25281
R:Williams, S.C.; Bruckheimer, S.M.; Lusis, A.J.; LeBeauf, R.C.; Kimbrough, A.J.
Mol. Cell. Biol. 6, 3807-3814, 1986
A:Title: Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-lipid diet
A:Reference number: A25281; MUID:87089722
A:Accession: A25281
A:Molecule type: DNA
A:Residues: 1-394 <WIL>
A:Cross-references: GB:M13966; NID:g192006; PIDN:AAA37253.1; PID:g387102
C:Genetics:
A:Introns: 16/1; 58/2
C:Superfamily: apolipoprotein A-I
;Keywords: chylomicron; HDL; lipid binding; lipoprotein

	Query Match	6.6%	Score 80.5;	DB 2;	Length 394;	
	Best Local Similarity	21.9%	Pred. No. 17;			
	Matches 39;	Conservative 41;	Mismatches 65;	Indels 33;	Gaps 77;	
QY	11 NSSLLLLLLSPCLR-----GTPDCYSHPSSISNFVKF---RELTDHL-----	53				
DQ	146 NTQGEKMDQLPYIRMQTTIKENVNDLHTSMPLAATLKDKFNRMNEELKGHLPRAN	205				
QY	54 -LKDYPTAVNLQDERHCKALMSLELAQRWTEQIKTVAGSKMOTLEDVNTLHEHYTSC	112				
DQ	206 RLK---ATIQNEDIEDRRSLAPLVAGEVKLNHQMEGLA-FQMKRNAEELYTKY---SA	257				
QY	113 TFGPRLPCFLAFQGTINSHLKDPCNQDALLAKRCICACAKONSFCLEVOCCPDSDSTLP	170				
DQ	258 KIDOL-----QKNLAPIVEDQSVKVGKNGETIGLOKALEDINKALKEQVEFRFTIYEP	308				

RESULT 22
A40892
apolipoprotein A-IV precursor - mouse (strain C57BL/6)
C:Species: Mus musculus (house mouse)
C:Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C:Accession: A40892
R:Reue, K.; Leete, T. H.
J. Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
A:Reference number: A40892, MUID:91286309
A:Accession: A40892
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <REU>
A:Cross-references: GB:M4249; NID:G19186; PIDN:AA37215.1; PID:G191867
A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
C:Keywords: lipid binding; lipoprotein

[illegible]

RESULT 23
E84527
hypothetical protein At2g15320 [Imported] - Arabidopsis thaliana
C1:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84527
C:Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C. Y
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon
euss, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: B84420; MUID:20083487
A:Accession: B84527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <STD>
A:Cross-references: GB:AE002093; NID:G4662629; PIDN:AAD26901.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g15320
A:Map position: 2

Query Match	6.5%	Score 80;	DB 2;	Length 382;
Best Local Similarity	24.7%	Pred. No. 18;		
Matches	53;	Conservative	18;	Mismatches 78; Indels 66; Gaps 8;

QY	14	LLLLLLLLSPCRGPDCCYFSSHPISSNKVKFRELTHLKDYPYTAVANIQDEKCKA	73
DB	4	LLLLLLL---LFSSADSLTSPSDVSA-----LKAFAKATVPKRNIPWSCA	47
QY	74	LMSLPLAQWIMIQLKTVAGSKMQTLLEDVNTFIHF-----VTSCTFOP-----	116
DB	48	SWDFTVSDPCASBPRT-----HFCGTCSSDSRTVQTLDPAGYNG	90
QY	117	-----LPECH--FVQINISHLKDTCTQLLAKPCIGKACONFSKCLEVOCPDSS	166
DB	91	RLTPLISGLTELLTDLAENNFGLIPSSISSTLSKLTILRS--NSFSGSL-----PDSV	144
QY	167	TLLPSPSIALEATELPEPRPROLLLLLLLLPLTL	201
DB	145	TRLNDSIESIDISNLTGPLPKTMNSLNIROLDL	179

RESULT 24

C40892

apolipoprotein A-IV precursor - mouse

C:Species: Mus musculus castaneus (southeastern Asian house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-1993

C:Accession: C40892

R:Reue, K.; Leete, T.H.

J. Biol. Chem. 266, 12715-12721, 1991

A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion

A:Reference number: A40892; MUID:91286509

A:Accession: C40892

A:Molecule type: mRNA

A:Residues: 1-399 <REU>

A:Cross-references: GB:M64250

A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 2

C:Superfamily: apolipoprotein A-I

C:Keywords: chylomicron; duplication; HDL; lipid binding; lipid transport; lipoprotein

Query Match	6.58;	Score 79.5;	DB 2;	Length 399;
Best Local Similarity	21.18;	Pred. No. 21;	Mismatches 69;	Indels 27;
Matches	37;	Conservative 42;	Gaps 6;	
QY	11	NSLSLLLLLSLSCLR-----GTPDCCFHSPSSNEKYAF-----RELTDHL--LK	55	
Db	147	NTQTOEKLTQLTPTTQIQMOTTIKENDNLHTSMPLATNLKDKFNNMBELKCHLPRAN	206	
QY	56	DYPTVAVNLQDERHCKATMSLFLAQRWTEQLKTVAGSKMQLLEQVNTLEIHFVYSCIQ	115	
Db	207	ELKATIDQNEDELRSLAPLTGVQVQEKLNQMGGLA-FQMKRAEELQTKV-----SAKID	261	
QY	116	PURECLRFVQTNTNLSHLKQTCQTLALMKPGICGAACNFSCHEVOCOPQSBSTLPP	170	
Db	262	QL-----QKNLAPLVEQVQSRVKGKGTGELQSKLDLNKQLEQVQDEERRRYVER	309	

RESULT	25
REASON	

T38299

probable beta-adaptin clathrin assembly protein - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03 Dec 1998
 C:Size: 1000
 C:Start: 1
 C:End: 1000

C/Species: Schizosaccharomyces pombe

```
C:\Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
```

C;Accession: T38299

R; Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.

submitted to the EMBL Data Library, September 1997

A; Reference number: Z21785

A;Accession: T38299

A;Status: preliminary; translated from GB/EMBL/DBJ

A:molecule type: DNA

A;Residues: 1-745 <SKE>

A;Cross-references: EMBL:Z99163; PIDN:CAB16234.1; GSPDB:GN00066; SPDB:SPAC23H3.06

A; Experimental source: strain 972h-; cosmid c23H3

C;Genetics:

A;Gene: SPDB:SPAC23H3.06

A;Map position: 1

A: Introns: 327/3

Query Match	6.5%	Score 79.5;	DB 2;	Length 745;
-------------	------	-------------	-------	-------------

Best Local Similarity 20.9%; Pred. No. 43;

Matches 62; Conservative 31; Mismatches 96; Indels 107; Gaps 13;

QY 16 LLLLLSPCLRGTPD-----CYFHSPISSNFKVKERELTDHLLKDYPTVA 62

Db 141 IVLLAIQCCITDTADRVRSALAITYCY - - - - SLDPYSKSQLEEHIKTLSDNSPIVP 196

QY 63 VNL-----QDEK-----HCKALWSLFLAQR-W--IEQLKTVAGSKMOTLLE-----100

Db 197 AALTFEEVVCPEKLEIHRYHRICTLFEPQNDWDKVALKTLVRYARLTLPPESTPSTH 256

QY 101 -DVNTEIHFTSCTFQPLPECL-----RVVQTNISHLKDTCTQLLALKPCIGKACQ 151

Db 257 SDLKELLESIKSCFESLLPSTIAGARAFYYLAPSNQMHLLIVEPLLQILLEKPIVRTTTL 316

QY 152 NF-----SRCLEVOQCQPDSSLLP----- 170

Db 317 RYISQIVYKTPLELFKNHKSFFLIASDSDDTCLKINILSRLLDAQ--NSSQILPELly 373

QY 171 -----PRSPALAE TEL-----PEPRRQ LLLLLLLPTV LLA AWGLR 211

Db 374 YINSHPNPSVASTAVKALGDEFASANISMAPSCINTLLLLKSHNSLIVTEAASSLR 4229

Search completed: August 6, 2002, 09:40:25
Job time: 216 sec

Job time: 216 sec

Gencore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: August 6, 2002, 09:46:19 ; Search time 16.81 Seconds

(without alignments)
532.077 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MVLAPAWSPNSLLILLLL.....WQARRRGELHGVLPSPHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1212.5	99.1	232	1 FL3L_MOUSE	P49772 mus musculus
2	768.5	62.8	235	1 FL3L_HUMAN	P49772; rat
3	89.5	7.3	841	1 GBR2_MOUSE	O75899 homo sapien
4	89	7.3	815	1 AD15_MOUSE	O88833 mus musculus
5	87	7.1	816	1 AD15_RAT	O88833; rat
6	84.5	6.9	1201	1 ATR3_HUMAN	O15077 adam 15 p
7	84	6.9	1409	1 AEX3_CAEL	O02626 caenorhabd
8	83.5	6.8	552	1 CSF1_MOUSE	P07144 mus musculus
9	83.5	6.8	2476	1 ZAN_PIG	O28983 sus scrofa
10	82.5	6.7	378	1 LEUK_RAT	P13838 rat
11	80.5	6.6	335	1 APA4_MOUSE	P06728 mus musculus
12	80	6.5	195	1 INT_OVIMO	P28172 ovibos mosc
13	79	6.5	1101	1 YAG_SCHPO	O09773 schistosac
14	78.5	6.4	122	1 YW2_MYCTU	O50691 mycobacteri
15	78.5	6.4	1208	1 RCG4_HUMAN	O94761 homo sapien
16	78.5	6.4	3068	1 PCG4_PEMVC	O01500 p genome po
17	78	6.4	224	1 CM35_HUMAN	O08708 homo sapien
18	78	6.4	806	1 SYEB_MYGE	P47433 mycoplasma
19	78	6.4	908	1 YN61_YEAST	P42839 saccharomyc
20	77.5	6.3	266	1 HB2D_CANFA	P18470 canis fami
21	77.5	6.3	940	1 GBR2_RAT	O88871 rattus norv
22	76.5	6.3	222	1 YB95_METHH	O02763 methanobact
23	76.5	6.3	336	1 VS09_ROTST	P03533 stigmat 11 r
24	76.5	6.3	1296	1 ASAL_EMMPA	P11533 enterococcu
25	76.5	6.3	3660	1 DM0_CHICK	P11533 gallus gall
26	76	6.2	438	1 PR11_DROME	O24311 drosophila
27	76	6.2	977	1 EYPA_MOUSE	O03145 mus musculi
28	75.5	6.2	379	1 CYB_CANDR	P24952 camelus dro
29	75.5	6.2	577	1 TRBM_MOUSE	P15306 mus musculi
30	75.5	6.2	4543	1 LRPI_CHICK	P98157 gallus gall
31	75	6.1	433	1 ENOA_SCEUN	O94712 sceioporus
32	75	6.1	513	1 AVR2_HUMAN	P27038 mus musculi
33	75	6.1	732	1 KELT_HUMAN	P23276 homo sapien

34	75	6.1	758	1 VKGC_HUMAN	P38435 homo sapien
35	75	6.1	887	1 SM6B_RAT	O70141 rattus norv
36	74.5	6.1	326	1 VS09_ROTST	P08406 porcine rot
37	74.5	6.1	356	1 TRBM_BOVIN	P06579 bos taurus
38	74	6.1	326	1 VS09_ROTST	P11855 human rotav
39	74	6.1	326	1 VS09_ROTST	P12476 rhesus rota
40	74	6.1	448	1 BCN1_MOUSE	O88597 mus musculi
41	74	6.1	450	1 BCN1_HUMAN	O14457 homo sapien
42	74	6.1	478	1 BM3B_HUMAN	P55107 homo sapien
43	74	6.1	513	1 AVR2_MOUSE	O28043 bos taurus
44	74	6.1	513	1 AVR2_MOUSE	P27038 mus musculi
45	74	6.1	818	1 DL13_HUMAN	O94777 homo sapien
46	74	6.1	818	1 TLRA_HUMAN	O94777 homo sapien
47	74	6.1	888	1 SM6B_HUMAN	O94777 homo sapien
48	74	6.1	1421	1 TIM_DROME	P49021 drosophila
49	73.5	6.0	415	1 TNR3_MOUSE	P50284 mus musculi
50	73.5	6.0	801	1 YEV7_YEAST	P40094 saccharomyc

ALIGNMENTS

RESULT	ID	FL3L_MOUSE	STANDARD	PRT	232 AA.
AC	P49772;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLR3 ligand).				
GN	FLR3LG OR FLR3L.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid-10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94195428; PubMed=8145851;				
RA	Hannum C., Culpepper J., Campbell D., McLanahan T., Zurawski S.,				
RA	Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luhn J.,				
RA	Mucha G., Melina N., Peterson D., Menon S., Shanafelt A.,				
RA	Duden M., Kellner G., Nankawa R., Renwick D., Roncarolo M.G.,				
RA	Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,				
RT	*Ligand for FLR3/FLK2 receptor tyrosine kinase regulates growth of				
RT	haematopoietic stem cells and is encoded by variant RNAs.;				
RL	Nature 368:643-648(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SU/J;				
RX	MEDLINE=94084791; PubMed=7505204;				
RA	Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,				
RA	Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,				
RA	Spielet R.R., Fletcher F.A., Maraskovsky E., Farrah T.,				
RA	Forwerthe D., Williams D.E., Beckmann M.P.;				
RT	*Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase				
RT	receptor: a proliferative factor for primitive hematopoietic cells.;				
RL	Cell 75:1157-1167(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96032581; PubMed=7566977;				
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,				
RA	Escobar S.;				
RT	*Structural analysis of human and murine flt3 ligand genomic loci.;				
RL	Oncogene 11:1165-1172(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95124710; PubMed=7824267;				
RA	Lyman S.D., James L., Escobar S., Downey H., de Vries P.,				
RA	Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,				
RA	Cleveland L.S.;				
RT	*Identification of soluble and membrane-bound isoforms of the murine				
RT	flt3 ligand generated by alternative splicing of mRNAs.;				

(IN SOLUBLE ISOFORM).
FT VARSPLIC 179 235 MISSING (IN SOLUBLE ISOFORM).
FT CONFLICT 72 72 G -> A (IN REF. 1).
SQ SEQUENCE 235 AA; 73b95b693b4CECF CRC64;

Query Match 62.8%; Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%; Pred. No. 1,2e-60;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY 1 MVLAPAMSPNSLLLLLSFCLRGTPDCYFSHSPISSNKRYKRELTHLKDYPVT 60
D 1 MVLAPAMSP-:::||||| | | | | | | | | | | | | | | | | | | | | |
1 MVLAPAMSP-:::||||| | | | | | | | | | | | | | | | | | | | | |
OY 61 VAVLQOEKCKALMSLFLAQRWIEQLKGVASCKMOTILEDVNTFHPVTSCTPCLPEC 120
D 60 VASLQDEELCGGLMRVLAQRMERKTVASCKMGLERVNTFHPVTCAPQPPSC 119
OY 121 LRFVQNIISHLKDTCTQLALPKICGACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
D 120 LRFVQNIISHLKDTCTQLALPKICGACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 177
OY 181 ELPEPRRQLLLLLPLTVLVAAGLWQORARR----GELHAPGVLP 228
D 178 APRAPQP-LLLLPLPGLLLLAACLMQRTTRRTPRGEOVPPVPS 227

RESULT 3
GBR2_HUMAN
ID GBR2_HUMAN STANDARD; PRT: 941 AA.
AC 075899; 075974; 075975; 09UNSR; Q9UNR1; Q9P1R2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B
51) (GPR 51) (HG20).
GN GABBR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
BA Barnes A.A., Emson P., Ford S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
GABA(B) receptor."
RL Nature 396:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS."
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G.,
HEZOG H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
with high affinity for GABA and low affinity for baclofen."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=fetal brain;

RX MEDLINE=99189236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
receptors expressed predominantly in nervous tissues and mapped
proximal to the hereditary sensory neuropathy type 1 locus on
chromosome 9".
RL Genomics 56:288-295(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
expression and coupling to adenylyl cyclase in the absence of
GABABR1".
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Elhier N., Hebert T.E., Sullivan R.,
Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
Mezey E., Johnson M.P., Liu Q., Kolakowski L.F., Jr., Evans J.F.,
Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
functional GABAB receptor activity".
RL J. Biol. Chem. 274:7607-7610(1999).
RN [8]
RP R1A-R2 INTERACTION.
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F., Jr.,
Johnson M.P., Hebert T.E., Elhier N., Bailey M., Welters K.,
Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
receptors with truncated receptors and metabotropic glutamate
receptor 4 supports the GABA(B) heterodimer as the functional
receptor".
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS. WHEREAS POSTSYNAPTIC
GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
ANTINOCICEPTION.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC EMBL; AJ012188; CAA09942.1; -
DR EMBL; AF056085; AAC63228.1; -
DR EMBL; AF095723; AAC63383.1; -
DR EMBL; AF095724; AAC63384.1; -
DR EMBL; AF095784; AAD30389.1; -
DR EMBL; AF074483; AAD03336.1; -
DR EMBL; AF069755; AAC99345.1; -
DR EMBL; AF099033; AAD4867.1; -
DR Interpro; IPR001828; ANF_receptor.
DR Interpro; IPR00337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 2.
DR PRINTS; PRO0248; GPCRMR.
DR PRINTS; PRO1176; GABAB2RECEPTR.
DR PRINTS; PRO1177; GABAB1RECEPTR.
DR PRINTS; PRO1178; GABAB2RECEPTR.
DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; FALSE_NEG.
DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; FALSE_NEG.
DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; FALSE_NEG.
DR PROSITE; PS50259; G_PROTEIN_RECEPT_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Postsynaptic membrane; Coiled coil; Alternative splicing;

FT	SIGNAL	.1	41	POTENTIAL.
FT	CHAIN	42	941	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2.
FT	DOMAIN	42	483	EXTRACELLULAR (POTENTIAL).
FT	TRANSHEM	484	504	I (POTENTIAL).
FT	DOMAIN	505	522	CYTOLASMIC (POTENTIAL).
FT	TRANSHEM	523	543	II (POTENTIAL).
FT	DOMAIN	544	551	EXTRACELLULAR (POTENTIAL).
FT	TRANSHEM	552	572	III POTENTIAL.
FT	DOMAIN	573	597	CYTOLASMIC (POTENTIAL).
FT	TRANSHEM	598	618	IV (POTENTIAL).
FT	DOMAIN	619	654	EXTRACELLULAR (POTENTIAL).
FT	TRANSHEM	655	675	V (POTENTIAL).
FT	DOMAIN	676	691	CYTOLASMIC (POTENTIAL).
FT	TRANSHEM	692	712	VI (POTENTIAL).
FT	DOMAIN	713	720	EXTRACELLULAR (POTENTIAL).
FT	TRANSHEM	721	741	VII (POTENTIAL).
FT	DOMAIN	742	941	CYTOLASMIC (POTENTIAL).
FT	DOMAIN	781	819	COILED COIL (POTENTIAL).
FT	CARBOHYD	80	90	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	404	404	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	453	453	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPPLIC	902	927	MISSING (IN ISOFORM 2B).
FT	VARSPPLIC	929	941	HPPSPFVMSGL -> TITLGRGVCCRRNVSQCEAGHHG MPPLPTTMMALRMTGRGRRLGT (IN ISOFORM 2C).
FT	VARANT	628	628	Y-> F.
FT	VARANT	628	628	/FTId=VAR_010148.
FT	VARANT	869	869	T-> A.
FT	CONFLICT	6	6	/FTId=VAR_010149.
FT	CONFLICT	12	12	S-> R (IN REF. 5).
FT	CONFLICT	424	424	P-> R (IN REF. 5).
EQ	SEQUENCE	941 AA.	105621 MM.	G-> E (IN REF. 3).
				09F1I73DB0673C5D CRC64;

Query Match	7.38;	Score 89.5;	DB 1;	Length 941;
Best Local Similarity	49.08;	Pred. No. 3;		
Matches	24;	Conservative	0;	Mismatches 16; Indels 9; Gaps 2;

QY 183 PEPRPRLLLLLLLPLTLVLLAAWGRLWRQRARRRGELHPGVLPSPH 231
| | | | | | | | | | | | | | |
, , , , , , , , , , , , , , ,

Db 15 PPPPPARLLLLL,PLLLPLAPGAWG---WARGAPR-----PPSSSP 54

RESULT	4
AD15_MOUSE	
ID	AD15_MOUSE
STANDARD;	
PRT;	815 AA.

DT 16-OCT-2001 (Rel. 4.0, Created)
DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
DT 01-MAR-2002 (Rel. 4.1, Last annotation update)
DE ADAM 15 precursor (NC 3,4,24-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDP-15) (Metalloprotease RGD disintegrin protein)
DE (Metalgadin) (AD55).
DE ADAM15 OR MDC15.
GN ADAM15
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A., AND INTRACELLULAR MATURATION.
RC TISSUE=Lung;
RX MEDLINE=98421554; PubMed=9748307;
RA Lum L., Reid M.S., Blobel C.P.;
RI "Intracellular maturation of the mouse metalloprotease disintegrin
RT MDC15.";
RT J. Biol. Chem. 273:26236-26247(1998).
TL

RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid, and Myeloma;
RA Shimizu E., Higuchi Y., Matsura K., Hijiya N., Yamamoto S.:
RT "Structure of the mouse ADAM 15 (AD6) gene."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RP INTERACTIONS WITH ENDOPHILIN I AND SORTING NEXIN 9.

RA Howard L., Nelson K.K., Maciewicz R.A., Blobel C.P.;

RT two SH3 domain-containing proteins, endophilin I and SH3PX1.";

CC -1- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS, CELL
FUNCTION AS TUMOR-ASSOCIATED PROTEIN ANTIGEN

CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

CC SORTING NEXIN 9. ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY BIND AND PROTECT THE NOT END PROTECTED BODY OF PLATE

CC SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE MAJORITY OF THE

CC CORRESPOND TO THE TRANS-GOLGI NETWORK OR THE LATE ENDOSOME. T

CC WHEREAS THE MAJORITY OF THE PROTEIN IN THE CELL IS PROCESSED.

CC KIDNEY. EXPRESSED AT LOWER LEVELS IN SPLEEN, LIVER, TESTIS AND

CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND

CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA5-BETA3 (BY

CC -|- PTH: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE. AN

ADDITIONAL MEMBRANE PROTEIN SITE OF CLEAVAGE AFFECTS A SMALL PERCENTAGE OF THE PROTEIN AND RESULTS IN DISULFIDE-LINKED

CC POSITIONS THAT ARE N-TERMINAL OF THE FURIN CLEAVAGE SITE.

```

-1- PTM: MAY BE PARTIALLY SIALYLATED.
CC
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC

```

CC -1- SIMILARITY: CONTAINS 1 EGFLIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN
CC -1- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC -----

between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its

DR PROSITE; PS0092; TSP1. 2.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
KM Hydrolase; Metalloprotease; zinc; Signal; Glycoprotein; Zymogen;
KM Repeat; Extracellular matrix; Heparin-binding.
FT NON_TER 1 1
FT SIGNAL <1 2
FT PROPEP 245
FT CHAIN 246 1201
FT METAL 394 394
FT ACT_SITE 395 395
FT METAL 398 398
FT METAL 404 404
FT DOMAIN 466 546
FT DOMAIN 547 603
FT DOMAIN 604 708
FT DOMAIN 709 840
FT DOMAIN 841 898
FT DOMAIN 899 961
FT DOMAIN 962 1013
FT DOMAIN 1013 245
FT CARBOHYD 79 79
FT CARBOHYD 115 115
FT CARBOHYD 238 238
FT CARBOHYD 341 341
FT CARBOHYD 471 471
FT CARBOHYD 810 810
FT CARBOHYD 938 938
SQ SEQUENCE 1201 AA; 135113 MW; D54BA92BD506A3AA CRC64;

Query Match 6.9%; Score 84.5; DB 1; Length 1201;
Best Local Similarity 21.9%; Pred. No. 11;
Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

QY 40 SNFKVFRRLTDLKDYPTVAVNIQDEKHKALMSFLAQRWIEQKTYAGSK----- 94
DB 872 SDDKVVRSCEANKKPKIRRMCMNQECTH-----PLWAEWHEHCRTGSSGYQLRT 926
QY 95 -MOTLLEVNTEHFV-----TSCFQPLP-----ECLRRV-QTNISH 130
DB 927 VRCLOPLDSTNSVSKYCMGDRPESRRPCNRVPCPMQWKTGWSSECVTGEGETEVR 986
QY 131 LT-----KDTCTOLLALPCIGKAC-----QNESRLEAYQC 161
DB 987 VLCRADHDCGKEPEVSRAQCLPNCDEPCLGDKSLFCQMEVLYARYSIPGNKLCESCC 1046
QY 162 QPSSSTLPPRSPIALETEL-----PEPPRQLLLLLLP 198
DB 1047 SKRSST-LPE--PYLLEAEHTHDVVISNPSDLPRSLVMPSTSLP 1087

RESULT 7
AEX3_CAEEL STANDARD; PRT; 1409 AA.
ID AEX3_CAEEL 027467;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of presynaptic activity aex-3.
GN AEX-3 OR CO2H7.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA MEDLINE=97282461; PubMed=9136770;
RA Iwasaki K., Staunton J., Saifee O., Nonet M., Thomas J.H.;
RT "aex-3 encodes a novel regulator of presynaptic activity in C.
elegans.";
RL Neuron 18:613-622(1997).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Reinbac D., Minx M.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP INTERACTION WITH CAB-1.
RX MEDLINE=20428446; PubMed=10970871;
RA Iwasaki K., Toyonaga R.;
RT "The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
in synaptic transmission.";
RL EMO J 19:4806-4816(2000).
CC -1- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR RAB3. MAY
REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.
CC -1- SUBUNIT: BINDS TO CAB-1.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
CC -1- SIMILARITY: CONTAINS 1 DENN DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC EMBL; U93842; AAB52421.1; -;
DR EMBL; U49945; AAC47926.1; -;
DR WormBep; CO2H7.3; CE16806.
DR InterPro; IPR001194; DENN.
DR Pfam; PF02141; DENN; 1.
KW Guanine-nucleotide releasing factor.
FT DOMAIN 216 364
FT DENN.
SQ SEQUENCE 1409 AA; 157458 MW; 2DDE6395AC963313 CRC64;

Query Match 6.9%; Score 84; DB 1; Length 1409;
Best Local Similarity 23.9%; Pred. No. 14;
Matches 54; Conservative 31; Mismatches 73; Indels 68; Gaps 13;

QY 4 LAPAMSPNSLLILLSPCLRGTPDCYFSHPISNFKVFRRL-TDHLKDYPTVA 62
DB 317 LTPAYWPSAE-QLLAPPLFLIGVPSFFNHR-----KIRELPSDVIYDLD-TNC 365
QY 63 VNIQDEKHKALMSFL-----AQRWIEQKTYAGSKMOTLLEDVNTE----- 105
DB 366 LQVPPD-----LITPDLPEPDATHLKERLKN-AIKMTTMTVDNETSVDADGIDT 416
QY 106 -----IHFVTS-----TPQPLECLRFVQTNISHLKDCTOTLALK 143
DB 417 DSDVDACRVAMVQFNPAVGFNFSEHTRRLRLYPVVSLOTDSFLRSRPOCTQLIT-D 475
QY 144 PCIGKACONEFSRCLEVOCA-PDSSSTLPPRSPIALETELPEPPR 188
DB 476 LCHTQAVETFAEC-----CLCPKNETFV--RVQAGIESAGVGDPK 515

RESULT 8
CSF1_MOUSE STANDARD; PRT; 552 AA.
ID CSF1_MOUSE P07141;
AC 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Macrophage colony stimulating factor-1 precursor (CSF-1) (M-CSF).
GN CSF1 OR CSFM.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090, 10116;
RN [1]

RP SPROUCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-87174763; PubMed-3494232;
 RA Delamarier J.F., Hession C., Semon D., Gough N.M., Rothenbuhler R.,
 RM Mermod J.-J.;
 RT "Nucleotide sequence of a cDNA encoding murine CSF-1
 (Macrophage-CSF).";
 RL Nucleic Acids Res. 15:2389-2390(1987).
 RN [2]
 RP SPROUCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-88320507; PubMed-2457916;
 RA Lader M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
 RM McGrogan M., Stanley E.R.;
 RT "cDNA cloning and expression of murine macrophage colony-stimulating
 factor from 1929 cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:6706-6710(1988).
 RN [3]
 RP SPROUCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-87147232; PubMed-3493488;
 RA Rajavashisth T.B., Eng R., Shaddock R.K., Waheed A., Ben-Avram C.M.,
 RM Shively J.E., Lusis A.J.;
 RT "Cloning and tissue-specific expression of mouse macrophage colony-
 stimulating factor mRNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1157-1161(1987).
 RN [4]
 RP SPROUCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-85242709; PubMed-3925458;
 RA Ben-Avram C.M., Shively J.E., Shaddock R.K., Waheed A.,
 RM Rajavashisth T.B., Lusis A.J.;
 RT "Amino-terminal amino acid sequence of murine colony-stimulating
 factor 1";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4486-4489(1985).
 RN [5]
 RP SPROUCE FROM N.A.
 RC SPECIES-RAT; STRAIN-WISTAR; TISSUE-Muscle;
 RX MEDLINE-93363632; PubMed-8357831;
 RA Borczyk A.G., Lemondard J., Guiller M., Lebovitch S.A.;
 RM "Isolation and characterization of a cDNA clone encoding for rat
 CSF-1 gene. Post-transcriptional repression occurs in myogenic
 differentiation";
 RL Biochim. Biophys. Acta 1174:143-152(1993).
 RN [6]
 RP SPROUCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-91340149; PubMed-1874443;
 RA Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
 RM Brockmeyer H.E.;
 RT "Cloning and characterization of the murine promoter for the colony-
 stimulating factor-1-encoding gene";
 RL Gene 102:165-170(1991).
 CC - FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC - FUNCTION: THIS CSF INDICES MACROPHAGES.
 CC - SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X05010; CAA28660.1; -
 DR EMBL; M21952; AAA37481.1; -
 DR EMBL; M21149; AAA37482.1; -
 DR EMBL; M15692; AAA37480.1; -
 DR EMBL; M84361; AAA03032.1; -

DR EMBL; M81316; AAA19856.1; -
 DR PIR; A23166; A23166.
 DR PIR; A26575; A26575.
 DR PIR; A31401; A31401.
 DR M01; M01:1339753; CSF1.
 RM cytokine; Growth factor; Glycoprotein; Signal.
 RT SIGNAL
 FT CHAIN 1 32
 FT DISULFID 33 552
 FT DISULFID 63 63
 FT DISULFID 39 122
 FT DISULFID 80 171
 FT DISULFID 134 178
 FT DISULFID 189 189
 FT DISULFID 191 191
 FT CARBOHYD 107 107
 FT CARBOHYD 154 154
 FT CARBOHYD 172 172
 FT VARIANT 292 292
 FT VARIANT 345 345
 FT CONFLICT 3 3
 FT CONFLICT 6 6
 FT CONFLICT 7 8
 FT CONFLICT 246 246
 SQ SEQUENCE 552 AA; 60648 MW; 3886D72D70E770AF CRC64;
 Query Match 6.8%; Score 83.5; DB 1; Length 552;
 Best Local Similarity 23.2%; Pred. No. 5.5;
 Matches 54; Conservative 36; Mismatches 94; Indels 49; Gaps 12;
 QY 12 SLLILLLLPCLRGTPDCYFSPSSNPFVKRELTDLHLKDYPTAVNLQDEKH-70
 DB 18 SLLVLLCMSRSIAKVESEHSCSHMIGNHLKV-IQQLIDSQM-ETSCQIAFEFVDEQL-75
 QY 71 ----CKALMSFLAQKRIEQL-----KYVAGSKMQLLEDVTEHFTSTQPLP-118
 DB 76 DDPVCYKKAFFLVQDITIDETMRKQNTPNANATETDELSSNNLV-----SCFTDYE-128
 QY 119 E----CLR-FVQT-----NISHLKTCTQLALPKCIGKACON-FSRC--LEVOGCPD-164
 DB 129 EQNKACVTRFTHPEPLQLLEKIKNFETFKMLLEKDMNIFTKCNNSFKCSRVVVRKP-188
 QY 165 SSTLLPRSPALAELEPPRRQLLLLLPLTLVYLLAAWGLRQRRAR-217
 DB 189 CNCYPRATPSSDPASAPHPAP-----SNAPLA-----GLANDDSOR-228
 RESULT 9
 ZAN_PIG STANDARD; PRT; 2476 AA.
 AC Q28983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Zonadhesin precursor.
 GN ZAN.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 RN [1]
 RP SPROUCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
 RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
 RP 1658-1667; 1777-1795 AND 1914-1921.
 RC STRAIN-MEISHAN; TISSUE-Testis;
 RX MEDLINE-96064658; PubMed-7592795;
 RA Hardy D.M., Gaiders D.L.;
 RT "A sperm membrane protein that binds in a species-specific manner to
 the egg extracellular matrix is homologous to von Willebrand
 factor";
 RL J. Biol. Chem. 270:26025-26028(1995).
 CC - FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
 OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR

CC SIGNALING.
 CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
 CC APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
 CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
 CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
 CC ZONA PELLUCIDA.
 CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
 CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
 CC SPERMATOZOEA OR PROMOTING ADHESION TO THE OVIDUCTAL Isthmus.
 CC -1- DOMAIN: THE WVED DOMAINS 2 AND 3 MAY MEDIATE COVALENT
 CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
 CC -1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
 CC FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
 CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
 CC CAPACITATION.
 CC -1- SIMILARITY: CONTAINS 2 MAM DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4.5 WVED DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U40024; AAC48486.1; -
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000998; MAM.
 CC InterPro: IPR002919; TIL.
 CC InterPro: IPR003328; TILA.
 CC InterPro: IPR001007; VMFC.
 CC InterPro: IPR001846; Vwd.
 CC Pfam: PF00629; MAM; 2.
 CC Pfam: PF01826; TIL; 5.
 CC Pfam: PF02345; TILA; 5.
 CC Pfam: PF00094; Vwd; 4.
 CC SMART: SM00181; EGF; 1.
 CC SMART: SM00137; MAM; 1.
 CC SMART: SM00214; WMC; 2.
 CC SMART: SM00216; WMD; 4.
 CC PROSITE: PS00022; EGF_1; 1.
 CC PROSITE: PS00186; EGF_2; 4.
 CC PROSITE: PS00740; MAM_1; 1.
 CC PROSITE: PS00650; MAM_2; 2.
 CC Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
 CC Repeat.
 CC KW
 CC FT SIGNAL 1 29 POTENTIAL.
 CC FT CHAIN 30 2476 ZONADHESIN.
 CC FT DOMAIN 30 2418 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 2419 2439 POTENTIAL.
 CC FT DOMAIN 2440 2476 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 31 144 MAM 1.
 CC FT DOMAIN 147 312 MAM 2.
 CC FT DOMAIN 319 687 53 x HEPTAPEPTIDE REPEATS (APPROXIMATE)
 CC (MUCIN-LIKE DOMAIN).
 CC FT DOMAIN 688 799 WVED 1 (PARTIAL).
 CC FT DOMAIN 800 1184 WVED 2.
 CC FT DOMAIN 1185 1573 WVED 3.
 CC FT DOMAIN 1574 1968 WVED 4.
 CC FT DOMAIN 1969 2370 WVED 5.
 CC FT DOMAIN 2366 2402 EGF-LIKE.
 CC FT DISULFID 2370 2381 BY SIMILARITY.
 CC FT DISULFID 2375 2390 BY SIMILARITY.
 CC FT DISULFID 2392 2401 BY SIMILARITY.
 CC FT CARBOHYD 109 2401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 735 735 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 738 738 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -----

FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1329 1329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1544 1544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1654 1654 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1843 1843 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1965 1965 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2122 2122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2165 2165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2178 2178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2329 2329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2359 2359 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 823 823 C -> V (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 923 923 S -> Y (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 965 965 W -> Y (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 1241 1241 S -> K (IN REF. 1; AA SEQUENCE).
 SO SEQUENCE 2476 AA; 270364 MW; A13869037546548C CRC64;
 Query Match 6.8%; Score 83.5; DB 1; Length 2476;
 Best Local Similarity 30.6%; Pred. No. 30;
 Matches 26; Conservative 12; Mismatches 32; Indels 15; Gaps 3;
 QY 144 PCIGKACQNFRCLE-----VQCC-----PDSSTLLPPRSPLATELPEPRPQLLL 193
 Db 2369 PCLNDPCQNDGRCREGGTHTCECELGYGGLCT-----EPGVPSPKPKPEASNVAILL 2423
 QY 194 LLLPLPTLVLLAAAGLRWGRARRR 218
 Db 2424 GMLMPVLVLPAYTRVSRRRRRR 2448
 RESULT 10
 LEUR_RAT
 ID LEUR_RAT STANDARD: PRT: 378 AA.
 AC P13838:
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leukostallin precursor (Leucocyte stialoglycoprotein) (Stialophorin)
 DE (CD43) (W3/13 antigen) (Fragment).
 GN SPN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=8816646; PubMed=2965006;
 RA Killeen N., Barclay A.N., Willis A.C., Williams A.F.;
 RT "The sequence of rat leukostallin (W3/13 antigen) reveals a molecule
 RT with O-linked glycosylation of one third of its extracellular amino
 RT acids".
 RL EMBO J. 6:4029-4034(1987).
 CC -1- FUNCTION: ONE OF THE MAJOR GLYCOPROTEINS OF THYMOCYTES AND T
 CC LYMPHOCYTES. PLAYS A ROLE IN THE PHYSICO-CHEMICAL PROPERTIES OF
 CC THE T-CELL SURFACE AND IN LECTIN BINDING. PRESENTS CARBOHYDRATE
 CC LIGANDS TO SELECTINS. HAS AN EXTENDED ROD-LIKE STRUCTURE THAT COULD
 CC PROTRUDE ABOVE THE GLYCOCALYX OF THE CELL AND ALLOW MULTIPLE
 CC GLYCAN CHAINS TO BE ACCESSIBLE FOR BINDING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, T LYMPHOCYTES,
 CC NEUTROPHILS, PLASMA CELLS AND MELOMAS.
 CC -1- PTM: HAS A HIGH CONTENT OF SIALIC ACID AND O-LINKED CARBOHYDRATE
 CC STRUCTURES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial


```

FT REPEAT 225 246 9.
FT REPEAT 247 268 10.
FT REPEAT 269 286 11.
FT REPEAT 287 308 12.
FT REPEAT 309 330 13.
FT DOMAIN 366 389 GLU/GLN-RICH.
FT VARIANT 382 385 MISSING (IN SOME STRAINS).
FT CONFLICT 15 15 MISSING (IN REF. 1).
FT CONFLICT 63 63 O -> K (IN REF. 1).
FT CONFLICT 207 207 E -> R (IN REF. 1).
FT CONFLICT 288 288 S -> A (IN REF. 1).
FT CONFLICT 294 295 RQ -> KA (IN REF. 1).
FT CONFLICT 315 316 NK -> GG (IN REF. 1).
SQ SEQUENCE 395 AA; 45029 MW; 5FE27D036226257 CRC64;

```

```

Query Match 6.6%; Score 80.5; DB 1; Length 395;
Best Local Similarity 21.1%; Pred. No. 6.9; Mismatches 69; Indels 27; Gaps 6;
Matches 37; Conservative 42;

```

```

QY 11 NSLLDLLLSPCLR-----GTPDCYFSPSSNFKVFP---RELTDLH--LK 55
DB 147 NQOEMKQLQLPYIQRMQTIKENVDLHTSMPLATNLKDKRNMEELKGLTPRAN 206
QY 56 DYPVAVANLQDEKCKRLNSLELAQKRWTEQKTVASKQMTLEEDVNTLHFTVSTCFQ 115
DB 207 ELKATIDNLEDRSLAPLVGVEKLNHMEGLA-FQMKKNMEELQTV---SAKID 261
QY 116 PLPECLRFVQTNISHLKDTCTQLATLKPICGACONFSCLEVOCCPSSTLIP 170
DB 262 QL-----QKNLAPLVEDQSKVKGNTGEGKSLIEDLNRLQLEQVEFFRTVTP 309

```

```

RESULT 12
INT_OVIMO STANDARD; PRT; 195 AA.
AC P28172;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antileuteolysin) (Trophoblast antileuteolytic protein).
GN IFN OR IFN.
OS Ovis aries moschatus (Muskoex).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovidos.
OX NCBI_TaxID=37176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; PubMed=1374107;
RA Leeman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox
RT and distribution of related genes among mammals.";
RL J. Interferon Res. 12:1-11(1992).
RN [2]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498;
RA Marital J.V., Chene N.M., Huynh L.P., L'Hartidon R.M., Reinaud P.B.,
RA Guillemot M.W., Charlier M.A., Charigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, a
RT non-ubiquitous expression, structure-function relationships, a
RT pregnancy hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
-1- FUNCTION: PARACRINE HORMONE PRIMARILY RESPONSIBLE FOR MATERNAL
RECOGNITION OF PREGNANCY. INTERACTS WITH ENDOMETRIAL RECEPTORS,
PROBABLY TYPE I INTERFERON RECEPTORS, AND BLOCKS ESTROGEN RECEPTOR
EXPRESSION, PREVENTING THE ESTROGEN-INDUCED INCREASE IN OXYTOCIN
RECEPTOR EXPRESSION IN THE ENDOMETRIUM. THIS RESULTS IN THE
SUPPRESSION OF THE PULSATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC
HORMONE PROSTAGLANDIN F2-ALPHA, HINDERING THE REGRESSION OF THE
CORPUS LUTEUM (LUTEOLYSIS) AND THEREFORE A RETURN TO OVARIAN

```

```

CC CYCLOTICITY. THIS, AND A POSSIBLE DIRECT EFFECT OF IFN-TAU ON
CC PROSTAGLANDIN SYNTHESIS, LEADS IN TURN TO CONTINUED OVARIAN
CC PROGESTERONE SECRETION, WHICH STIMULATES THE SECRETION BY THE
CC ENDOMETRIUM OF THE NUTRIENTS REQUIRED FOR THE GROWTH OF THE
CC CONCEPTUS. IN SUMMARY, DISPLAYS PARTICULARLY HIGH ANTIVIRAL AND
CC ANTIPROLIFERATIVE POTENCY CONCURRENTLY WITH PARTICULAR WEAK
CC CYTOTOXICITY, HIGH ANTILEUTEOLYTIC ACTIVITY AND IMMUNOMODULATORY
CC PROPERTIES. IN CONTRAST WITH OTHER IFNS, IFN-TAU IS NOT VIRALLY
CC INDUCIBLE.
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE UTERINE LUMEN.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY AND EXCLUSIVELY EXPRESSED IN
CC THE MONONUCLEAR CELLS OF THE EXTRA-EMBRYONIC TROPHOCTODERM.
CC -1- DEVELOPMENTAL STAGE: MAJOR SECRETORY PRODUCT SYNTHESIZED BY THE
CC CONCEPTUS DURING A VERY SHORT PERIOD IN EARLY PREGNANCY.
CC -1- MISCELLANEOUS: IFN-TAU GENES ARE INTERLOUS. THEY EVOLVED FROM
CC IFN-OMEGA GENES IN THE RUMINANTIA SUBORDER AND HAVE CONTINUED TO
CC DUPLICATE INDEPENDENTLY IN DIFFERENT LINEAGES OF THE RUMINANTIA.
CC THEY ENCODE FOR PROTEINS VERY SIMILAR IN SEQUENCE BUT WITH
CC DIFFERENT BIOLOGICAL POTENCY AND PATTERN OF EXPRESSION.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY. IFN-ALPHA1 SUBFAMILY.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M73244; AAA31583.1; -.
CC HSSP: P01563; 2HE.
CC Interpro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS: PR00266; INTERFERONAB.
CC ProDom: PD000550; Interferon_abd. 1.
CC SMART: SM00076; IFabd. 1.
CC PROSITE: PS00252; INTERFERON_A_B_D. 1.
CC pregnancy; Cytokine; Hormone; Antiviral; Signal; Glycoprotein.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 195 INTERFERON TAU.
CC FT DISULFID 24 122 BY SIMILARITY.
CC FT DISULFID 52 162 BY SIMILARITY.
CC FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 195 AA; 22370 MW; 39599512F3C34208 CRC64;

```

```

Query Match 6.5%; Score 80; DB 1; Length 195;
Best Local Similarity 27.4%; Pred. No. 3.5;
Matches 34; Conservative 17; Mismatches 33; Indels 40; Gaps 7;

```

```

QY 13 SLLLLLLSPCLRTPTCYFSPHP---ISSNFKV--KREITDH----- 52
DB 6 SLKMLVAVSTCPGSGSLACYLSRRPTLDVRENLRDLDMNRLSHSCQDQKPGFQEM 65
QY 53 -----LKDQPVTV-----AVNLQDEKCKRLNSLELAQKRWTEQKTVASKQMTLE 100
DB 66 VEGDQLQDQDALSVLYEMLQGRFNLFTHEHSCAMNTTL-----LEQART--GLHQQ--LE 117
QY 101 DYNF 104
DB 118 DLDL 121

```

```

RESULT 13
YAAG_SCHPO STANDARD; PRT; 1101 AA.
AC 009733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 126.5 kDa protein C31A2.16 in chromosome 1.
GN SPAC31A2.16.

```

```

OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DB).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC
DR EMBL: Z50113; CA90474.1;
DR InterPro: IPR000219; RhGEF.
DR Pfam: PF00621; RhGEF; 1.
DR SMART: SM00325; RhGEF; 1.
DR PROSITE: PS00741; DH_1; FALSE_NEG.
DR PROSITE: PS50010; DH_2; 1.
DR Hypothetical protein.
KM DOMAIN 230
FT SEQUENCE 1101 AA; 126537 MW; B26C47589F76F50B CRC64;
SQ
Query Match 6.5%; Score 79; DB 1; Length 1101;
Best Local Similarity 20.0%; Pred. No. 30;
Matches 42; Conservative 32; Mismatches 66; Indels 70; Gaps 8;
OY 37 PISNKKVKKRETLIDLD-----YPTVANVLDDEKHCAL---WSLFQGRW 83
DB 815 PLSKEKEITGSDLDYDNLKETNEELLISHYPPNI-IVATFOKYLSSFINRKGVLSSSF 873
OY 84 IEOLKTVAGSKMOTLLEDVN---TEIHFTVSCFPOPLPECLRFVQTNISHLKDTQTQ 138
DB 874 IQQLNTV-----ENLNLSFNSSTDVAYHKLKIQDLPESSKLLENIFSIASD--- 920
OY 139 LALKKPCIGKACQNSRCLEVOGCPDS-----STLPPRSP 175
DB 921 -LLRLRLPLKDQCFVTKQIALALAPSMEGSNAVELYIAYHSRIFSTVEELPTPVSPA 979
OY 176 -----ALEATELPEPRROL 191
DB 980 NSNNKQLDSEKFOALAMKEMPERHPKXIL 1009
RESULT 14
YMW2_MYCTU STANDARD; PRT; 122 AA.
ID YMW2_MYCTU
AC 050691;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.9 kDa protein RV2272.
GN RV2272 OR MT2333 OR MTCY339.38C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

```

```

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RT Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weisman J., Khouri H., Gill J., Mikala A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO E.COLI YIDH.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC
DR EMBL: Z77163; CAB00963.1;
DR EMBL: AE007076; AAK46616.1;
DR TIGR: MT2333;
DR Tuberculist; RV2272;
DR InterPro: IPR03807; DUF202.
DR Pfam: PF02656; DUF202; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 33 53
FT TRANSMEM 58 78
FT TRANSMEM 97 117
FT SEQUENCE 122 AA; 12994 MW; 23A5375426487A7 CRC64;
SQ
Query Match 6.4%; Score 78.5; DB 1; Length 122;
Best Local Similarity 33.0%; Pred. No. 2.8;
Matches 29; Conservative 12; Mismatches 24; Indels 23; Gaps 5;
OY 162 QPD-SSTLPPRSPALAEAT-----ELPEPRROLILLPLPTLVLL 204
DB 13 EPDYRTFLANERTFLAWORTALGLAAVAALVQVPELTIFGAROVGLVLAI---LAIL 69
OY 205 AAAMG-LRWQARRRGELHPVPLRSH 231
DB 70 TSGMGLRWQADRAMRRH--LPLRPH 95
RESULT 15
RCO4_HUMAN STANDARD; PRT; 1208 AA.
ID RCO4_HUMAN
AC 094761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-dependent DNA helicase Q4 (RecQ protein-like 4).
GN RECQ4 OR RCO4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99097344; PubMed=9878247;
RA Kitao S., Ohsugi I., Ichikawa K., Goto M., Furuiichi Y., Shimamoto A.,

```


RT "Cloning of two new human helicase genes of the recQ family:
 RT biological significance of multiple species in higher eukaryotes.";
 RL Genomics 54:443-452(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20021764; PubMed-10552928;
 RA Kihao S., Lindor N.M., Shalstori M., Furuchi Y., Shimamoto A.;
 RT "Rothmund-Thomson syndrome responsible gene, RECQL4: genomic structure
 RT and products.";
 RL Genomics 61:268-276(1999).
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- DISEASE: DEFECTS IN RECQL4 ARE A CAUSE OF ROTHMUND-THOMSON
 CC SYNDROME (RTRS). A DISEASE CHARACTERIZED BY DERMATOLOGICAL FEATURES
 CC SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY
 CC ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
 CC DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
 CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB006532; BAA74453.1; -
 CC EMBL: AB026546; BAA6899.1; -
 CC MIM: 603780; -
 CC MIM: 268400; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam: PF00270; DEAD.1.
 DR Pfam: PF00271; helicase_C.1.
 DR SMART: SM00487; DEXDC.1.
 DR SMART: SM00490; HELIC.1.
 DR SMART: SM00343; ZnF_CZHC.1.
 KW Hydrolyase; Helicase; ATP-binding; Nuclear protein.
 FT NP_BIND 509
 FT SITE 605 608 DEAD BOX.
 FT SEQUENCE 1208 AA; 13076 MW; CB809A7765AB48A1 CRC64;
 SQ
 Query Match 6.4%; Score 78.5; DB 1; Length 1208;
 Best Local Similarity 22.8%; Pred. No. 37;
 Matches 66; Conservative 27; Mismatches 111; Indels 85; Gaps 13;
 QY 9 SPNSLL-LLLLSPCLNGTPCYTS--HSPIS--SNPKYKRELDHLKIDPV 59
 DB 523 SPCLTIVSPILSIMDQVSGLPCKACIHSGRKQRESVLQKIRAAOVHVLMTPE 582
 QY 60 T-----VAVNLDEKHCKALMSLFLAQRILEOLKTV----- 90
 DB 583 ALVAGGLPPAAOLPVAFACIDBAHCLSQSHNFRPYLRCKYKLVREMGVHCFGLTA 642
 QY 91 -----AGSKMOTLEDVNFNEIHVYISCTROPLECLRFVQVOTNISHL---KDCITQL 140
 DB 643 TATRTATADVAOHVAEEDPLH-----GPAF-----VPTNL-HLSYSDMRDIDCAL 689
 QY 141 ALKPCIGACONFS-----RCLEVOCCPDSSSTLLPPRSPTALEAT 180
 DB 690 TLLQ--GKRFQNDLSIIYCNRRREDTERIALRLTILHAAMVPGSGGRAPKTTAAVHAG 747
 QY 181 ELPEPRPQLLLLLPLTVLLAAMGLRMQRRRREGELHPGVPLS 229
 DB 748 MCSRRR-RRVQRAFMQGLRVVATVAFMGGLDRPRVAVLHLGLP-PS 794

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Genome polypeptide [Contains: N-terminal protein (p1); Helper
 DE component proteinase (EC 3.4.22.-) (HC-PRO); Protein p3; 6 kDa protein
 DE 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2);
 DE Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (NIA)
 DE (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-PRO); Nuclear inclusion
 DE protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
 DE Coat protein (CP)].
 OS Pepper mottle virus (California isolate) (PepMV) (Pepov C).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
 OC Polyvirus.
 OX NCBI_TaxID=31737;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93033110; PubMed-1413501;
 RA Vance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;
 RT "The complete nucleotide sequence of pepper mottle virus genomic RNA:
 RT comparison of the encoded polypeptide with those of other sequenced
 RT polyviruses.";
 RL Virology 191:19-30(1992).
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: Hydrolyses glutamyl bonds, and activity is
 CC further restricted by preferences for the amino acids in p6 - p1'
 CC that vary with the species of polyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
 CC Glu+Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -1- PFM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PFM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M96425; AAA46903.1; -
 CC PIR: A44062; A44062.
 DR MEROPS: C04.001; -
 DR MEROPS: C06.001; -
 DR MEROPS: S30.001; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR001730; Peptidase_C4.
 DR InterPro: IPR001456; Peptidase_C6.
 DR InterPro: IPR002540; Poly_P1.
 DR InterPro: IPR001592; Poly_coat.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00270; DEAD.1.
 DR Pfam: PF00271; helicase_C.1.
 DR Pfam: PF00863; Peptidase_C4.1.
 DR Pfam: PF00863; Peptidase_C6.1.
 DR Pfam: PF00767; Poly_coat.1.
 DR Pfam: PF01577; Poly_P1.1.
 DR Pfam: PF00680; RNA_dep_RNA_pol.1.
 DR PRINTS: PR00966; NIAPOTYPTASE.
 DR SMART: SM00487; DEXDC.1.

DR SMART; SM00490; HELIC; 1.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 287 N-TERMINAL PROTEIN.
 FT CHAIN 288 743 HELPER COMPONENT PROTEINASE.
 FT CHAIN 744 744 PROTEIN P3.
 FT CHAIN 1157 1156 6 KDA PROTEIN 1.
 FT CHAIN 1157 1790 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1791 1842 6 KDA PROTEIN 2.
 FT CHAIN 1843 2276 GENOME-LINKED PROTEIN.
 FT CHAIN 2277 2795 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2796 3068 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 1906 COVALENT LINKAGE OF VIRAL RNA
 (BY SIMILARITY).
 FT NP BIND 1241 1248 ATP (POTENTIAL).
 FT SEQUENCE 3068 AA; 348651 MW; FD3458B837FDA7C2 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 3068;
 Best Local Similarity 25.4%; Pred. No. 1.1e+02;
 Matches 31; Conservative 19; Mismatches 61; Indels 11; Gaps 5;

OY 37 PISSENFVKRELTDHLK-DY-PTVAVANLQDEK---HCKALMSFLAQRMIEOLKTV 90
 1612 PLSES-SIFRASSDWITAGDYRIGVYKIDIPEDIRIFHKTFRKFTNNMESVLYKTK 1670
 OY 91 AGSKMQLLEDVTEHFEVTSCTFQPLPECLRFVQTNISHLKDTCTQLLAKPCIGKAC 150
 1671 ASAFPLTRSSITKIAVLTSTDLVAIPRLTAVES---LLEDEKTKOYQFSLIDNGC 1726
 OY 151 ON 152
 Db 1727 SS 1728

RESULT 17
 CM35_HUMAN STANDARD; PRT; 224 AA.
 ID CM35_HUMAN
 AC 008708;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE CMR35 antigen precursor.
 GN CMR35.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249405; PubMed=1349532;
 RA Jackson D.G., Hart D.N.J., Starling G., Bell J.I.;
 RT "Molecular cloning of a novel member of the immunoglobulin gene
 RT superfamily homologous to the polymorphic immunoglobulin receptor."
 RL Eur. J. Immunol. 22:1157-1163(1992).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- TISSUE SPECIFICITY: PRESENT ON THE SURFACE OF MONOCYTES,
 CC NEUTROPHILS, A PROPORTION OF PERIPHERAL BLOOD T AND B LYMPHOCYTES
 CC AND LYMPHOCTIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; X66171; CAA46948.1; .

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 KW Antigen; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 224
 FT DOMAIN 21 183 CMR35 ANTIGEN.
 FT TRANSMEM 184 204 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 205 224 POTENTIAL.
 FT DOMAIN 36 117 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 123 175 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 123 175 PRO-RICH.
 FT DISULFID 43 110 POTENTIAL.
 FT DISULFID 57 65 POTENTIAL.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 99 99 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 224 AA; 24830 MW; 60C8871BD84600D2 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 224;
 Best Local Similarity 23.1%; Pred. No. 6.1;
 Matches 60; Conservative 27; Mismatches 89; Indels 84; Gaps 12;

OY 5 APAPNSLSLLILLISLSELCGTPDCYFSRSPISNFKYFRELTDHLKDYPTVA-- 62
 3 ARAMASMRSSALLILLVPG-----YF---PLS-----HPMTVACP 34
 OY 63 -----VNIODEHCKAL--W-----SLFLAQRMIEOLKTVAGSKMQLLEDVTEHFEV 109
 35 VGSLSVQCRYEKEHEHRTLTKFKCRRPQTLRCDKIVETKGSAGKRNQVSTRSPANLSTF- 93
 OY 110 TSCFTQPLPECLRFVQTNISHLKDTCTQLLAL-----KPCIGKACONFSRCLEVO 160
 94 -TVTLENLITE-----EDAGTYMCGVDPFWLRFDFHPIVEVSVPAQTTRA 139
 OY 161 COPDSS-----TLPPRSPIALEATELPEPRP-----ROLILLILLPLFLVTL 204
 140 SSFQSSMGTSGPPTKLPVTPMPSVTRKSDPPSPHPSLSNVRFLLVLEPLLSML 199
 OY 205 AAA-WGIWMQARRRNGELHP 223
 Db 200 GAVLWVNRPRQSSRSRQWMP 219

RESULT 18
 STFB_MYCGE STANDARD; PRT; 806 AA.
 ID STFB_MYCGE
 AC P47437; Q49516;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phenylalanine-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
 DE tRNA ligase beta chain) (PheRS).
 GN PHE1 OR MG195.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmales; Mycoplasma.
 OX NCBI_Taxid=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Eult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fitchman J.L., Weidman J.F., Small K.V., Sandusky M., Furman J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.F., Dougherty B.A., Bolt K.F., Hu P.-C., Lueder T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RU Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 1-94 AND 682-798 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M29611: AAA30874.1; -.
 DR PIR: A45844; A45844.
 DR HSSP: P13760; ZSEB.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR ProDom: PD000328; MHC_II_beta; 1.
 DR SMART: SM00407; IGcl; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW MHC II: Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 266
 FT DOMAIN 30 124 DLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
 FT DOMAIN 125 227 DR-1 BETA CHAIN.
 FT TRANSMEM 228 250 EXTRACELLULAR BETA-2.
 FT DOMAIN 251 266
 FT DISULFID 44 108 CYTOPLASMIC TAIL.
 FT DISULFID 146 202 BY SIMILARITY.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 266 AA; 30151 MW; 4E8297BBF1ACDD67 CRC64;
 Query Match 6.38; Score 77.5; DB 1; Length 266;
 Best Local Similarity 19.98; Pred. No. 8.2;
 Matches 55; Conservative 52; Mismatches 92; Indels 77; Gaps 12;
 QY 4 LAPAMSPNSLLILLILSP---CLRGNP-----DCYFHSPISSNFKYKRELTMD 51
 Db 7 LGGSM--TALMLILVNLNPPFAMAROTPPHLEVANSSECFY---NGTERVREVERYT 60
 QY 52 HLKDY-----PYTVAVNLQDE-----KCKKALMSLFLA 80
 Db 61 HNRREFVAFDSVGEFRAVTELRGPAVESNMGQKEILQERATVDYCRNNGVTESEFTV 120
 QY 81 QRWIEQLKTVAGSKMQLILEVDNTEIHFTVIST---FQPLDECLREYQTN-----IS 129
 Db 121 QRREPTVTVYPTKQTL-----QHNNLAVCSVNGFYPGHIEVRMIRNGQEEAGVYST 174
 QY 130 HLK--DTCTQLALKPCIGKACONFSRCLEVOCPDSSTLLPERSPIALEATELPEPRP 187
 Db 175 GLINGNDWTFQILVLELIVPQSGEYIT-----CQVEHPSL--TSPTVYEMRAQSDSAQ 225
 QY 188 RQLLLLLLLPLTLVLLAAWGLRWQARRRGELAP 223
 Db 226 SKMLSGIGGFVLGLFLAVGLFIERNQKGHSGLQP 261
 RESULT 21
 GBR2_RAT STANDARD; PRT; 940 AA.
 ID GBR2_RAT
 AC O88871; O90WU2; O9JTK36;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE gamma-aminobutylic acid type B receptor, subunit 2 precursor (GABA-B
 receptor 2) (GABA-B-R2) (Gb2) (GABABR2).
 GN GABBR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hypothalamus;
 RX MEDLINE=99087320; Pubmed=9872315;
 RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,

RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
 RA Salom J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
 RA Brachek T.A., Gerald C.;
 RT "GABA(B) receptors function as a heteromeric assembly of the subunits
 RT GABA(B)1 and GABA(B)R2.";
 RL Nature 396:674-679(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain cortex, and Cerebellum;
 RX MEDLINE=99087322; Pubmed=9872317;
 RA Kaupmann K., Maltsevsk B., Schuler V., Heid J., Froestl W., Beck P.,
 RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
 RA Beller B.;
 RT "GABA-B receptor subtypes assemble into functional heteromeric
 RT complexes.";
 RL Nature 396:683-687(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=20193514; Pubmed=10727622;
 RA Clark J.A., Mezey E., Lam A.S., Bonner T.L.;
 RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
 RL Brain Res. 860:41-52(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RA Borowsky B., Laz T., Gerald C.;
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP R1A-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
 RC TISSUE=Hypocampus;
 RX MEDLINE=99102694; Pubmed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of heteromer formation in GABA-B Receptor function.";
 RL Science 283:74-77(1999).
 CC -I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTIINDUCEDCEPTION.
 CC -I- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
 CC CEREBELLUM, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
 CC CEREBELLUM.
 CC -I- DEVELOPMENTAL STAGE: ABUNDANT IN BRAIN CORTEX AND CEREBELLUM
 CC THROUGHOUT POSTNATAL DEVELOPMENT WHEREAS ITS EXPRESSION IN SPINAL
 CC CORD GRADUALLY DECREASES.
 CC -I- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

[illegible]

```

CC Methanothermobacter.
OX NCBI_TaxID=145262;
RA SMITH D.R., Doucette-Stamm L.A., DeJonghery C., Lee H.-M., Dubois J.,
RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Jiwani N., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Saffer H., Patwell D., Prabhakar S.,
RA McDonnell S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT J. Bacteriol. 179:7135-7155(1997).
RL -1- SIMILARITY: TO M.JANNASCHII MJ1481.
CC -----
CC The SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/).
CC or send an email to license@sib-ch.ch).
DR EMBL: AE000887; AAB85684.1;
KW Hypothetical protein; Complete proteome.
SV SEQUENCE 222 AA; 24863 MW; A5FADDE6657CEA94 CRC64;
QY Query Match 6.3%; Score 76.5; DB 1; Length 222;
Dd Best Local Similarity 24.8%; Pred. No. 8.1;
Dd Matches 37; Conservative 21; Mismatches 50; Indels 41; Gaps 6;
QY 47 RELDHLKQYPYPAVAVNLQDEKHCALMSFLQOR-WIEOLTKVAGSKMQTLL----- 99
Dd 78 READDHILADFGVLEKQDSEIRIRKAGSKLLIVNNSVKKLTKAGVQKQNLVAGAPL 137
QY 100 -----EYVNEIHFTVTSCTFQPLPE-CIRFQYQTNISHLADTCYQLAKLPCTGKACQNF 153
Dd 138 SYVDMRIRINKI-----PESALRGIEKKITEHLRNDIERKDALDEVL----- 179
QY 154 SRCLEVCQPDSSLTLLPPRSPIALATEL 182
Dd 180 -----VVGEPDKSTVL-----LAARAEEL 198
RESULT 23
VS09_ROT51 STANDARD; PRT; 326 AA.
AC P03533;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein VP7 (Serotype-specific antigen) (Outer shell
DE glycoprotein).
GN S9.
OS Simian 11 rotavirus (strain SA11-Both).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=37137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83221547; PubMed=6304692;
RA Both G.W., Matlick U.S., Beilamy A.R.;
RT "Serotype-specific glycoprotein of simian 11 rotavirus: coding
RT assignment and gene sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3091-3095(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84165100; PubMed=6323768;
RA Arias C.F., Lopez S., Bell J.R., Strauss J.H.;
RT "Primary structure of the neutralization antigen of simian rotavirus

```

```
CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.  
CC -|- SIMILARITY: TO OTHER STREPTOCOCCAL AND STRAPHYLOCOCCAL PROTEINS  
IN THE REGION OF THE MEMBRANE ANCHOR.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@sib-sib.ch).  
-----  
CC  
DR EMBL; X17214; CAA35083.1; -.  
DR PIR; S10223; HMSOLF.  
DR InterPro; IPRO01899; Gram_pos_anchor.  
DR Pfam; PF00746; Gram_pos_anchor; 1.  
DR Prosite; PS00343; GRAM_POS_ANCHORING; 1.  
KW Plasmid; Transmembrane; Cell wall; Signal.  
FT SIGNAL 1 43  
FT CHAIN 1 43  
FT FT 44 1296 AGREGATION SUBSTANCE.  
FT DOMAIN 44 1268 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1269 1289 MEMBRANE ANCHOR.  
FT DOMAIN 1290 1296 CYTOPLASMIC (POTENTIAL).  
FT FT 1223 1260 CELL WALL REGION (PROBABLE).  
FT DOMAIN 1261 1266 CONSERVED IN GRAM-POSITIVE COCCI SURFACE  
FT FT PROTEINS.  
FT SEQUENCE 1296 AA; 142285 MW; 52123A133AD23E5B CRC64;  
  
Query Match 6.3%; Score 76.5; DB 1; Length 1296;  
Best Local Similarity 20.8%; Pred. No. 60;  
Matches 41; Conservative 29; Mismatches 62; Indels 65; Gaps 9;  
  
QY 38 ISSNFKPEFELDHLKDYPVAVNODCKHCKALMSFLQAQRMIEOLKTVAASKMOT 97  
Db 1149 ISKLFMTFFQSQSVKTTASQAFLDMLNKKNNVAHSKAKFG--VERI-AAAGVYNT 1203  
QY 98 LLEDVNTETHEFTVSCTEQPLPECLRFVOYN--ISHLLKIDTCYTLAIKPCIGAKCNFSR 155  
Db 1204 IEESFNNE-----KIKTNVTHTPE-----KP----- 1226  
          :::|::|:  
QY 156 CLEVOCPDSSTLLPR-----SPALE--ATELPERRPOLLLLLLPTVL 203  
Db 1227 ----QPREPKTVVPRTPKTPQAPVEPLVERKASVVELQTGEKNVLTLYAGSLAML 1282  
QY 204 LAAMGLRMORANFRGE 220  
Db 1283 GLAGLG----KERKE 1294  
               ::|  
  
RESULT 25  
DMD_CHICK STANDARD; PRT; 3660 AA.  
ID DMD_CHICK  
AC F11333;  
DT 01-OCT-1989 (rel. 12, Created)  
DT 01-OCT-1989 (rel. 12, Last sequence update)  
DT 01-MAR-2002 (rel. 41, Last annotation update)  
DE Dystrophin.  
GN DMD.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8909831; PubMed=3062582;  
RA Iemaike C., Heilig R., Mandel J.L.;  
RL "Nucleotide sequence of chicken dystrophin cDNA.";  
RL Nucleic Acids Res. 16:11815-11815(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;
```

```

RX MEDLINE-89210800; PubMed-3072195;
RA Lemaitre C., Heilig R., Mandel J.L.;
RT "The chicken dystrophin cDNA: striking conservation of the C-terminal
RT coding and 3' untranslated regions between man and chicken.";
RL EMBL J. 7:4157-4162(1988).
CC -!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYOSKELETON TO THE
CC PLASMA MEMBRANE.
CC -!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIBRIN,
CC ABP-120, ABP-180, OR BETA-FODRIN).
CC -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC -!- SIMILARITY: CONTAINS 22 SPECTRIN REPEATS.
CC -!- SIMILARITY: CONTAINS 1 WW DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL: X13369; CAA31746.1; -.
DR PIR: S02041; S02041.
DR HSSP: P46939; 1BHD.
DR InterPro: IPR001589; Actinin_act_bind.
DR InterPro: IPR001715; Calponin_hom.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001202; WW.
DR InterPro: IPR002349; WW_domain.
DR InterPro: IPR000433; Znf_ZZ.
DR Pfam: PF00307; CH; 2.
DR Pfam: PF00435; spectrin; 22.
DR Pfam: PF00397; WW; 1.
DR Pfam: PF00569; Zz; 1.
DR PRINTS: PR00403; WMDOMAIN.
DR SMART: SM00033; CH; 2.
DR SMART: SM00150; SPEC; 21.
DR SMART: SM00456; WW; 1.
DR SMART: SM00291; Znf_ZZ; 1.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS00020; ACTININ_2; 1.
DR PROSITE: PS50021; CH; 2.
DR PROSITE: PS01159; WW_DOMAIN_1; 1.
DR PROSITE: PS50020; WW_DOMAIN_2; 1.
DR PROSITE: PS01357; ZF_ZZ_1; 2.
DR PROSITE: PS01357; ZF_ZZ_2; 1.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat; Zinc-finger.
FT DOMAIN 1 244 ACTIN-BINDING.
FT DOMAIN 19 123 CH 1.
FT REPEAT 138 241 SPECTRIN 1.
FT REPEAT 341 449 SPECTRIN 2.
FT REPEAT 450 558 SPECTRIN 3.
FT REPEAT 561 669 SPECTRIN 4.
FT REPEAT 721 830 SPECTRIN 5.
FT REPEAT 832 936 SPECTRIN 6.
FT REPEAT 945 1047 SPECTRIN 7.
FT REPEAT 1050 1156 SPECTRIN 8.
FT REPEAT 1159 1265 SPECTRIN 9.
FT REPEAT 1268 1369 SPECTRIN 10.
FT REPEAT 1470 1570 SPECTRIN 11.
FT REPEAT 1573 1678 SPECTRIN 12.
FT REPEAT 1681 1782 SPECTRIN 13.
FT REPEAT 1879 1981 SPECTRIN 14.
FT REPEAT 2013 2103 SPECTRIN 15.
FT REPEAT 2106 2211 SPECTRIN 16.
FT REPEAT 2214 2321 SPECTRIN 17.
FT REPEAT 2472 2574 SPECTRIN 18.
FT REPEAT 2577 2683 SPECTRIN 19.
FT REPEAT 2686 2799 SPECTRIN 20.
FT REPEAT 2802 2904 SPECTRIN 20.

```

```

FT REPEAT 2906 2928 SPECTRIN 21.
FT REPEAT 2931 3037 SPECTRIN 22.
FT DOMAIN 3052 3085 WW.
FT ZN_FING 3304 3351 Z2-TYPE.
FT VARIANT 1171 1171 MISSING.
FT VARIANT 1869 1869 0 -> H.
FT VARIANT 1885 1885 K -> R.
SQ SEQUENCE 3660 AA; 422874 MW; 85493DAF6D5B6D4A CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 3660;
Best Local Similarity 24.6%; Pred. No. 1.9e+02;
Matches 52; Conservative 37; Mismatches 83; Indels 39; Gaps 12;

QY 31 CYSHSPISNNKVKRRELTDHLKDY--PYVAVNLODEKHCALMSLFLAQRWITQLK 88
DB 3337 CFPS-GRVAKGHMHP-----WVEYCTPTTSGEDVD--FAVVLKKRFTKRYFAKHP 3387
QY 89 TVAGSKMOTLEEDVNTETIHFVTSCTFOPLECFREVOFNISHLKDTQTLALKP--C 145
DB 3388 RMGYLPVQTVLEGDNNETP-VTLINFWPVDALAMENSGSYLNDISIPNESIDDEHL 3446
QY 146 IGAACQNFRCLEVCQPDSSSTLLPPRSP---TALERTPEPRPRQLLLLLPLTL 201
DB 3447 IQHYCQSLNQ-----ESPLSOPRSPAOITLISEERGE-----LERILLADLEEN 3492
QY 202 VLLAAMGLRWQRRRRGELHPGV-PLPSHP 231
DB 3493 RNLA---EYDLKQOHD-HKGLSPLPSP 3518

```

Search completed: August 6, 2002, 09:46:22
Job time: 403 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:45:49 ; Search time 47.12 Seconds

(without alignments)
848,086 Million cell updates/sec

Title: US-09-448-378-2
1223

Sequence: 1 MVTIAPAMSPNSLLILL.....MORARRGELHPVPLPSHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP rivirus: *
16: SP bacteriap: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.9	71.9	172	11 061104	061104 mus musculu
2	779.5	63.7	292	6 09GKE0	09gke0 bos taurus
3	774	63.3	294	6 09MZV0	09mzv0 canis fam11
4	761	62.2	291	6 09MZU9	09mzu9 felis silve
5	678.5	55.5	274	6 09GKD9	09gkd9 bos taurus
6	95.5	7.8	909	10 042484	042484 arabidopsi
7	94	7.7	355	4 09H665	09h665 homo sapien
8	93.5	7.6	510	6 09BGV6	09bgv6 macaca fasc
9	90.5	7.4	909	10 09ASPS	09asps arabidopsi
10	88.5	7.2	326	12 083443	083443 murine rota
11	88.5	7.2	326	12 083448	083448 murine rota
12	88	7.2	258	4 09H563	09h563 homo sapien
13	88	7.2	765	4 094824	094824 homo sapien
14	88	7.2	843	4 014584	014584 homo sapien
15	87.5	7.2	1254	5 09VFS1	09vfi1 drosophila
16	87.5	7.2	477	11 09CYB2	09cyb2 mus musculu

17	87.5	7.2	1231	10 09FKE2	09fke2 arabidopsi
18	87	7.1	1256	5 09VFS0	09vfi0 drosophila
19	86.5	7.1	2111	5 091802	091802 drosophila
20	86.5	7.1	4167	5 09GPN8	09gpn8 drosophila
21	86	7.0	962	5 096164	096164 plasmodium
22	85	7.0	181	5 017726	017726 caenorhabd1
23	85	7.0	1305	2 006521	006521 enterococcu
24	85	7.0	4513	10 09MBP8	09mbf8 chlamydomon
25	84.5	6.9	364	4 096AV5	096av5 homo sapien
26	84.5	6.9	939	16 09KOC8	09koc8 vibrio chol
27	84	6.9	330	5 09H4U7	09h4u7 caenorhabd1
28	83.5	6.8	588	8 09B6D1	09b6d1 yarrowia 11
29	83	6.8	258	4 09UMT2	09umt2 homo sapien
30	83	6.8	267	5 09W2D7	09w2d7 drosophila
31	83	6.8	1059	5 09VNP5	09vnp5 drosophila
32	82.5	6.7	326	12 085032	085032 porcine rot
33	82.5	6.7	326	12 085034	085034 porcine rot
34	82.5	6.7	335	8 092Y32	092y32 orycteropu
35	82.5	6.7	379	8 09T799	09t799 tapirus ind
36	82.5	6.7	431	10 09SN38	09sn38 arabidopsi
37	82.5	6.7	809	11 09DBY4	09db4 mus musculu
38	82.5	6.7	1266	10 09XET3	09xet3 lycopersico
39	82	6.7	575	10 09L568	09l568 arabidopsi
40	81.5	6.7	659	4 09H9U7	09h9u7 homo sapien
41	81.5	6.7	1148	4 09H6W7	09h6w7 homo sapien
42	81.5	6.7	7201	5 09VMT8	09vmt8 drosophila
43	81	6.6	348	8 09SA24	09sa24 conger myrl
44	81	6.6	2721	4 09B283	09b283 homo sapien
45	81	6.6	2721	4 096L90	096l90 homo sapien
46	81	6.6	4131	5 019542	019542 caenorhabd1
47	80.5	6.6	326	12 056347	056347 murine rota
48	80.5	6.6	326	12 083441	083441 murine rota
49	80.5	6.6	395	11 09DBN0	09dbn0 mus musculu
50	80.5	6.6	395	11 091XF8	091xf8 mus musculu

ALIGNMENTS

RESULT 1
061104 PRELIMINARY; PRT; 172 AA.
ID 061104;
AC 061104;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FLT3 LIGAND, T169 FORM.
GN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Mattson J., Tsai S., Luh J., Gutmares M.J., Mattei M.G., Rosnet O.,
RA Birnbaum D., Hannum C.,
RT "flt3 ligand: expression, genomic organization, alternatively spliced
forms and processing.",
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44024; AAA93305.1; -
DR MGD; MGI:95560; FLT3L.
DR InterPro; IPR004213; flt3_lig.
DR Pfam; PF02947; flt3_lig; 1.
SQ SEQUENCE 172 AA; 19465 MW; 04FOA010171E3384 CRC64;

Query Match 71.9%; Score 879; DB 11; Length 172;
Best Local Similarity 98.2%; Pred No. 1.1e-82;
Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MVTIAPAMSPNSLLILLSPCLRGTPDCYPSHSPISNFKVFKREITDHLKDPVT 60
|||||

Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDYPT 60
 QY 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 Db 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTL 168
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTL 168

RESULT 2

Q9GKE0 PRELIMINARY; PRT; 292 AA.

AC Q9GKE0 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DE FLT3 LIGAND ISOFORM-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Mwangi W., Brown W.C., Palmer G.H.;
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF9322.1; -;
 DR InterPro; IPR004213; flt3_1lg.
 DR Pfam; PF02947; flt3_1lg.1;
 SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match

Best Local Similarity 63.7%; Score 779.5; DB 6; Length 292;
 Matches 165; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDYPT 60
 Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDYPT 60
 QY 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 Db 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 180
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 180
 QY 181 ELPEPR-PROLILLLPLTVLVAANGL-RWQARRR----- 218
 Db 179 SLFGPSPILLILLLILVALILATAMWLCRMRRRRRTYRGERRTLRPRESSHLP 238
 QY 219 -----GELHPGVLPSPHP 231
 Db 239 DRESELGSSQLPEP-PFLGHP 258

RESULT 3

Q9MZV0 PRELIMINARY; PRT; 294 AA.

AC Q9MZV0 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE FLT3 LIGAND.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF155148; AAF67088.1; -;
 SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match

Best Local Similarity 63.3%; Score 774; DB 6; Length 294;
 Matches 158; Conservative 23; Mismatches 38; Indels 6; Gaps 4;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDYPT 60
 Db 1 MTVLAPAMSPNS-LLLLLLSPGLRGTPDCSFHSPSSNSTFAVTIRKSLDYLLQDYPT 59
 QY 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 Db 60 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 119
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 180
 Db 120 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 177
 QY 181 ELPEPR-PROLILLLPLTVLVAANGL-RWQARRR----- 224
 Db 178 ALPAPAPR-LLILLPLVALILMSTWCLMRRRRRRRSPRPG 220

RESULT 4

Q9MZU9 PRELIMINARY; PRT; 291 AA.

AC Q9MZU9 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE FLT3 LIGAND.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF155149; AAF87089.1; -;
 SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match

Best Local Similarity 62.2%; Score 761; DB 6; Length 291;
 Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPSSNFYKFKRELTDHLKDYPT 60
 Db 1 MTVLAPAMSPNTS-LLLLLLSPGLRGTPDCSFHSPSSNSTFAVTIRKSLDYLLQDYPT 59
 QY 61 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 120
 Db 60 VAVNLQDEKHKALMSLFLAQRMWIEQLKTVAGSKMOTLLEDVNTFHFVTSCTFOPLPEC 119
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 180
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPTALEAT 180

DB 120 LRFVQTNISHLQDTSBQLAKPWTR--RNFSGCLEQCQPDSTPLPRSPALAEAT 177
QY 181 ELPEPRRQLLLLLLLLLPTLVLLAAWGLRWARRR 218
DB 178 ALPAPQ-APLLLLLLPVALLLMSAAWCLHMRRRWR 214

RESULT 5
O9GKD9 PRELIMINARY; PRT; 274 AA.

ID O9GKD9
AC O9GKD9
DT 01-MAR-2001 (TREMUREL. 16, Created)
DT 01-MAR-2001 (TREMUREL. 16, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE FLI3 LIGAND ISOFORM-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570936; PubMed=11120823;
RA Mwangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (FLI3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL: AF282986; AAR99323.1; -.
DR InterPro: IPR004213; flt3_1lg.
DR Pfam: PF02947; flt3_1lg; 1.
SQ SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match 55.5%; Score 678.5; DB 6; Length 274;
Best Local Similarity 57.5%; Pred. No. 8.2e-62;
Matches 150; Conservative 19; Mismatches 41; Indels 51; Gaps 6;

QY 1 MTVALPAMSPSSLLLLLLSPCLRTGPCYSHSPISNFKVRFELTDHLKDYPT 60
DB 1 MTVALPAMSPPTSLLLLLSPCLQSTPCSPSHSPSTFAIKLGKLSKYLLODYPVT 60
QY 61 VAVNLQDEKCKALMSLFLAQRWIEQLKTVAGSKMOTLEEDVTEHFTVSCFQPLREPC 120
DB 61 VASNLQDDKLCGAFWRILYLQAWMGRLKTVAGSEMEKLEEDVTEHFTVSCAFQ----- 115
QY 121 LRFVQTNISHLKDTCTQQLALKPCIGKACONFSRCLEVOCCDSSLLPRSPALAEAT 180
DB 116 -----DTHQDLKLPWT--TRNFSKCLELQCPDSTPLDLPSPGALGAT 160
QY 181 ELPEPR-RPQLLLLLLPTLVLLAAWGL-RWQARRR----- 218
DB 161 SLFGPQSLLLLLLLPVALLLATAWCLCHWRRRRTYRPGERRTLRPRESSHLPA 220
QY 219 -----GELHGPVLPSPHP 231
DB 221 DTESLGGSQLPFG-PLGHP 240

RESULT 6
O42484 PRELIMINARY; PRT; 909 AA.

ID O42484
AC O42484
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE RPS2 (DISEASE RESISTANCE PROTEIN RPS2).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=col-0;
RC MEDLINE=9437978; PubMed=8091210;
RA Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R.,
RA Giraudat J., Leung J., Staskawicz B.J.;
RT "RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant
RT disease resistance genes."
RL Science 265:1856-1860(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95007758; PubMed=7923358;
RA Mindinos M., Katagiri F., Yu G., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats."
RL Cell 78:1089-1099(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Bevan M., Rose M., Hempel S., Entian K.-D., Hoheisel J., Mewes H.W.,
RA Mayer K.F.X., Scheller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EV Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA EV Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: U14158; AA21874.1; -.
DR EMBL: U12860; AA50236.1; -.
DR EMBL: AL049483; CAB39674.1; -.
DR EMBL: AL161564; CAB79464.1; -.
DR InterPro: IPR001687; ATP_GMP_A.
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR; 4.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERISIT.
SQ SEQUENCE 909 AA; 104640 MW; D279B6E30E49D640 CRC64;

Query Match 7.8%; Score 95.5; DB 10; Length 909;
Best Local Similarity 22.8%; Pred. NO. 0.36; Indels 57; Gaps 11;
Matches 53; Conservative 40; Mismatches 89;

QY 14 LLLLLLSPCLNGTPDCYFSHPISNFKVRFELTD-----HLKDYPTVA----- 62
DB 535 LTTLMQLQNSLKKIPTFGFHMPYLRYDLSTFSTIEPLSIKLYELVHLMSGGRIS 594
QY 63 -----VNLQDEKCKALMSLFL-----AQRWIEQLKTV-----AGSKMOTLEEDVNT 104
DB 595 VLPQELGNLKKLKHLDLQRTQFLQTPRDALCWLKLEYLVNLYSYAGMEQLSGEDPAE 654
QY 105 EIHPE-----VTSCTFQPLPECLRF--VQTNISHLKDTCTQQLALK-PCIGK 148
DB 655 ELGFADLEYLNTTGLGITVLSLETILKTLFEGALHKHIOHJHVECEMELLYFWLPSLTN 714
QY 149 ACONFSRCLEVOCCDSSLLPRSPALAEATLPRPRLULLLLPTLVLLAAW 208
DB 715 HGRNLR-LSIKSCHLEYLV---TPADFNWLPSS---LEVTLHSHNLTRY-----W 762
QY 209 G 209
DB 763 G 763

RESULT 7

	Only Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
	Matches	41;	Conservative	15;	Mismatches	59;	Indels	84;	Gaps
Qy	116	PLPE-----CLRFVOTNLSHLNDTCYQOLLAKRC-----IGKAC-----QNESECL	157						
Db	18	PPPPASGYCRLRYMNPNDKNCSSCLORGRPPCCDYFRENCGLNHDGFVTPPFKKS	77						
Qy	158	EVQCGPPSSLTLP-----	171						
Db	78	SGGCGNPPGAELCSCTCGGGAVTPPPAAGGRTWRRCRRPVPKAGHCPLTPGNPGAPSSQE	137						
Qy	172	RSPIALEATLPEPRPRQ-----LTLTLTLPLTVLLAAMGLRQWRARRGE	220						
Db	138	RSSVASSIAWRTEPEPQQAAMPNPLPLVVLVLTLLTAVIALTLFTLLMHLQWPKRADPY	197						
Qy	221	LHPGV-----PLPSH	230						
Db	198	PYPGLVCGVNPNTTPSSSH	216						

RESULT	8		
Q9BGY6			
ID	Q9BGY6	PRELIMINARY:	PRT: 510 AA.
AC	Q9BGY6;		
DT	01-JUN-2001 (Tremblrel, 17, Created)		
DT	01-JUN-2001 (Tremblrel, 17, Last sequence update)		
DT	01-DEC-2001 (Tremblrel, 19, Last annotation update)		
DE	HYPOTHEITICAL 56.5 KDA PROTEIN.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=FRONTAL LOBE LEFT;		
RA	Oseida N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,		
RA	Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Isolation of full-length cDNA clones from macaque brain cDNA		
RT	libraries."		
RL	Submitted (FEb-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB055271; BAB21895.1; -		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR003592; LRR_out.		
DR	InterPro; IPR003591; LRR_tyr.		
DR	Pfam; PF00560; LRR_6		
DR	PRINTS; PR00019; LEURICHRPT.		
DR	SMART; SM00370; LRR; 4.		
DR	SMART; SM00369; LRR_tyr; 6.		

```

0Y 9 SPNSLLLLLLLLPCLKTRP-----CYSHSPISNKKVFEIREIOTHL 53
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db STNLSLFLNALLSLSRNGIEVGEDALDGLMTLRTLLEHNOISS-----SLDHTF 103

0Y 54 --LKQDPYVAWV-----LODE--KHCKALMSFLAQRMWIEOL--KTVAGSMOTL--LE 100
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db SKLHSLQVVLVSNMNLRTLRGSEWRNRTGLRLQDLOGNOITNLITSSSGGNLMSLKHND 163

0Y 101 DWNTEIHFVYSCFPRIPECLARVQTN-----ISHLKD-----TCROLL 140
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db LSNMFSTYICKDAFRLRL--LOEVDLSNRLAMHPVFTPLKOLITLSLDKNQMSCTCDL 222

0Y 141 ----ALKPCIGKACONFSKLEVOCCOPDSSTLLPPRSPIALEATELEPEPRROLL-- 193
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db HPLARELRNYIKSSAFTLRNADKLNDCOPSTIAAAAAOYLRSETKCDPKRANFTLVKLD 262

0Y 194 -LLDLP-----LTVYLLAAAWGL-----RWQARRRGEIIL 222
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db RSPLLPQGVALLTVYLGFGAAGVLCGLGVFNKKLDOOGCANDH 326

```

```

Q9ASP5      9      PRELIMINARY;      PRT;      909 AA.
ID   Q9ASP5
AC   Q9ASP5
DT   01-JUN-2001 (TREMBLrel. 17, Created)
DT   01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   DISEASE RESISTANCE PROTEIN RPS2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eumariophyta; Viridiplantae; Streptophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX   NCBI_Taxid=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21231631; PubMed=11333251;
RA   Banerjee D., Zhang X., Bent A.F.;
RT   "The leucine-rich repeat domain can determine effective interaction
RT   between RPS2 and other host factors in Arabidopsis RPS2-mediated
RT   disease resistance.";
RL   Genetics 158:439-450(2001).
DR   EMBL; AF368301; AAK38117.1; -.
DR   InterPro: IPR003593; AAA.
DR   InterPro: IPR001687; ATP_GTP_A.
DR   InterPro: IPR007675; Disease_resist.
DR   InterPro: IPR001611; LRR.
DR   InterPro: IPR002182; NB-ARC.
DR   Pfam; PF00560; LRR; 4.
DR   Pfam; PF00931; NB-ARC; 1.
DR   PRINTS; PR00364; DISEASERISIT.
DR   SMART; SM00382; AAA; 1.
DR   SMART; SM00370; LRR; 4.
SQ   ATP-binding.
KW   SEQUENCE      909 AA; 104613 MW; F83E0F881B409DFA CRC64;

```

```
Query March      7.43; Score 90.5; DB 10; Length 909;
Best Local Similarity 22.8%; Pred.No.1.2;
Matches 53; Conservative 36; Mismatches 91; Indels 57; Gaps 11.;
```



```

RP      SEQUENCE FROM N.A.
RA      Waterston R.;
RL      Submitted (FE7-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AC0003077; AAB83946.1; -.
DR      InterPro; IPR000194; ATPase_alpha_beta.
DR      PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
FT      NON-TER      1      1
FT      NON-TER      843      343
SQ      SEQUENCE      843 AA; 97965 MW; 41DFA877D4D64725 CRC64;

Query Match      7.2%; Score 88; DB 4; Length 843;
Best Local Similarity 20.1%; Pred. No. 2;
Matches 51; Conservative 29; Mismatches 56; Indels 116; Gaps 14.;

QY      27 GMPDCYFHSPTSSNPKYKRELTHLKL---DYPTVAVNIQDEKHCALM---STFL 79
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      483 GVPD-----NIKSYKY-----NHMKFRDRFRPHKGT-KDKEEFSLWVERTSYL 529

QY      80 AQ-----RW-IEDLKTAVGSKMOT---LLEDVNTETI-HFYTSC-----TFQPLPEL 121
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      530 VQSLPGISWFEVEKREYVEMSPLENAIEVLNNKNOQLKTLISOCOTROMONINPLTML 589

QY      122 -----RFV 124
      : | | |

DB      590 NGVIDAANVGVSRRQEAFFVEKYEIILSHPEDGKAIARLRLMDEQAQLLEFGIAVEKTV 649

QY      125 GTNISHLLKDTGTLALRPGIGKACQNSRCLEVO-----CO-----PDS 165

```

Best Local Similarity	20.1%;	Pred. No. 1.8;			
Matches	51; Conservative	29; Mismatches	58; Indels	116; Gaps	14;

```
QY      166  STLLPPRSPIALEA 179
          :  :  |  |  |  :  |
Db      708  TRVTPRRSPLSYPA 721

PRESITT 15
```

Q9VE51 ID PRELIMINARY; PRT; 1254 AA.

AC	Q24742	01-MAY-2000	(TEMBLrel. 13, Created)
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)	
DT	01-MAY-2000	(TEMBLrel. 13, Last annotation update)	
DT	01-OCT-2001	(TEMBLrel. 18, Last annotation update)	

DE CG6045 *Proteinase B* (Fruit f1v)
GN CG6045 *Proteinase B* (Fruit f1v)

US Dirosophila melanoscela; 22422 22423 22424 22425 22426 22427 22428 22429 22430 22431 22432 22433 22434 22435 22436 22437 22438 22439 22440 22441 22442 22443 22444 22445 22446 22447 22448 22449 22450 22451 22452 22453 22454 22455 22456 22457 22458 22459 22460 22461 22462 22463 22464 22465 22466 22467 22468 22469 22470 22471 22472 22473 22474 22475 22476 22477 22478 22479 22480 22481 22482 22483 22484 22485 22486 22487 22488 22489 22490 22491 22492 22493 22494 22495 22496 22497 22498 22499 22500 22501 22502 22503 22504 22505 22506 22507 22508 22509 22510 22511 22512 22513 22514 22515 22516 22517 22518 22519 22520 22521 22522 22523 22524 22525 22526 22527 22528 22529 22530 22531 22532 22533 22534 22535 22536 22537 22538 22539 22540 22541 22542 22543 22544 22545 22546 22547 22548 22549 22550 22551 22552 22553 22554 22555 22556 22557 22558 22559 22560 22561 22562 22563 22564 22565 22566 22567 22568 22569 22570 22571 22572 22573 22574 22575 22576 22577 22578 22579 22580 22581 22582 22583 22584 22585 22586 22587 22588 22589 22590 22591 22592 22593 22594 22595 22596 22597 22598 22599 22600 22601 22602 22603 22604 22605 22606 22607 22608 22609 22610 22611 22612 22613 22614 22615 22616 22617 22618 22619 22620 22621 22622 22623 22624 22625 22626 22627 22628 22629 22630 22631 22632 22633 22634 22635 22636 22637 22638 22639 22640 22641 22642 22643 22644 22645 22646 22647 22648 22649 22650 22651 22652 22653 22654 22655 22656 22657 22658 22659 22660 22661 22662 22663 22664 22665 22666 22667 22668 22669 22670 22671 22672 22673 22674 22675 22676 22677 22678 22679 22680 22681 22682 22683 22684 22685 22686 22687 22688 22689 22690 22691 22692 22693 22694 22695 22696 22697 22698 22699 22700 22701 22702 22703 22704 22705 22706 22707 22708 22709 22710 22711 22712 22713 22714 22715 22716 22717 22718 22719 22720 22721 22722 22723 22724 22725 22726 22727 22728 22729 22730 22731 22732 22733 22734 22735 22736 22737 22738 22739 22740 22741 22742 22743 22744 22745 22746 22747 22748 22749 22750 22751 22752 22753 22754 22755 22756 22757 22758 22759 22760 22761 22762 22763 22764 22765 22766 22767 22768 22769 22770 22771 22772 22773 22774 22775 22776 22777 22778 22779 22780 22781 22782 22783 22784 22785 22786 22787 22788 22789 22790 22791 22792 22793 22794 22795 22796 22797 22798 22799 22800 22801 22802 22803 22804 22805 22806 22807 22808 22809 22810 22811 22812 22813 22814 22815 22816 22817 22818 22819 22820 22821 22822 22823 22824 22825 22826 22827 22828 22829 22830 22831 22832 22833 22834 22835 22836 22837 22838 22839 22840 22841 22842 22843 22844 22845 22846 22847 22848 22849 22850 22851 22852 22853 22854 22855 22856 22857 22858 22859 22860 22861 22862 22863 22864 22865 22866 22867 22868 22869 22870 22871 22872 22873 22874 22875 22876 22877 22878 22879 22880 22881 22882 22883 22884 22885 22886 22887 22888 22889 22890 22891 22892 22893 22894 22895 22896 22897 22898 22899 22900 22901 22902 22903 22904 22905 22906 22907 22908 22909 22910 22911 22912 22913 22914 22915 22916 22917 22918 22919 22920 22921 22922 22923 22924 22925 22926 22927 22928 22929 22930 22931 22932 22933 22934 22935 22936 22937 22938 22939 22940 22941 22942 22943 22944 22945 22946 22947 22948 22949 22950 22951 22952 22953 22954 22955 22956 22957 22958 22959 22960 22961 22962 22963 22964 22965 22966 22967 22968 22969 22970 22971 22972 22973 22974 22975 22976 22977 22978 22979 22980 22981 22982 22983 22984 22985 22986 22987 22988 22989 22990 22991 22992 22993 22994 22995 22996 22997 22998 22999 23000 23001 23002 23003 23004 23005 23006 23007 23008 23009 23010 23011 23012 23013 23014 23015 23016 23017 23018 23019 23020 23021 23022 23023 23024 23025 23026 23027 23028 23029 23030 23031 23032 23033 23034 23035 23036 23037 23038 23039 23040 23041 23042 23043 23044 23045 23046 23047 23048 23049 23050 23051 23052 23053 23054 23055 23056 23057 23058 23059 23060 23061 23062 23063 23064 23065 23066 23067 23068 23069 23070 23071 23072 23073 23074 23075 23076 23077 23078 23079 23080 23081 23082 23083 23084 23085 23086 23087 23088 23089 23090 23091 23092 23093 23094 23095 23096 23097 23098 23099 23100 23101 2310

CC Ephyraeidae; Pluteiellidae; Pteropoda;
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
RX MEDLINE-20196006; PubMed-10731132;
Fungal C 1 Coccyzus J D

RA Adams M.D., Cealnikner S.E., Holt R.A., Evans C.N., Socciante S.P.,
RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Chao I.Y.

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Y., Chen D.A.,
RA Brandton R.C., Rogers J.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA
Abiril J.F., Agbanyani A., An H.-J., Andrews-pinnakoch C., Balawan D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R.A. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkowicz D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA

RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.T., Harvey D., Heitman T.J., Hernandez J.R., Houck J.,

RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Harris R.D., Havelka T., Johnson J., Jones S., Karpman P., Kline
M., Ladd G., Leach A., Lewis J., Long B., Macdonald W., McQuinn
K., Miller J., Mitchell J., Nadeau J., O'Connell J., O'Neil J., O'Neil
J., O'Neil J., O'Neil J., O'Neil J., O'Neil J., O'Neil J., O'Neil J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon S., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rehner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitslks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 CC -1 - COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
 DR EMBL: AE003709: AAF55209.1: -.
 DR FLYbase: FBgn0038349: CG6045.
 DR Interpro: IPR002888: 2fe-2s_BD.
 DR Interpro: IPR000564: 2fe2s_ferredoxin.
 DR Interpro: IPR000674: Aldxan_dh.C.
 DR Interpro: IPR002346: dehydrog_molyb.
 DR Interpro: IPR001041: Ferredoxin.
 DR Pfam: PF01315: Ald_xan_dh.C; 2.
 DR Pfam: PF02738: Ald_xan_dh.C2; 1.
 DR Pfam: PF00941: PAD binding_5; 1.
 DR Pfam: PF00111: fer2; 1.
 DR Pfam: PF01799: fer2_2; 1.
 DR PRODOM: PD186071: 2fe-2s_BD; 1.
 DR PROSITE: PS00197: 2FE2S_FERREDOXIN; 1.
 KW Iron-sulfur.
 SQ SEQUENCE 1254 AA; 13786 MW; 4CC7F24F15D80851 CRC64;

Query Match 7.2%; Score 88; DB 5; Length 1254;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 39; Conservative 23; Mismatches 53; Indels 62; Gaps 7;

QY 21 LSPCLNGTPDCYFSHPISNFE-----VKKRELTID-----HLKDYP 58
 DB 655 LQPSL---GDVFASPTSPSSRIVPASKSKIKRSEDPKENVGICPMGQIYFTMEPQ 711
 QY 59 VIVYAVLQDEKCKALMSFLAQRWIEQLKYAGSKMGTLEEDVNTETI----- 107
 DB 712 TVVALPEFEG-----LKIFSATQMDQTOVIAHMLQVKKADVOLQVRLGGGYGSKIT 765
 QY 108 -----FVTSCTFOPLPECLRFVQTNISHLKDCTCTLLAKPCIGK--ACONFSRC 156
 DB 766 RGNQVACASLVAYKLNRPVRVQS-----LESMDNCGRMKRACRSDYKC 810
 RESULT 16
 Q9CYB2 PRELIMINARY; PRT; 477 AA.
 AC Q9CYB2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 5730557B1SRK PROTEIN.
 GN 5730557B1SRK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischman W., Gaasterland T., Gissi C., King B., Kochi H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK017844: BAB30970.1: -.
 DR HSSP: P42773: 11HB.
 DR MGD: MGI:1917904: 5730557B1SRK.
 DR Interpro: IPR002110: ANK.
 DR SMART: SM00248: ANK_4.
 DR PROSITE: PS00086: ANK_REPEAT; 1.
 DR PROSITE: PS50297: ANK_REPEAT_REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 477 AA; 52119 MW; 95AA4CF3891B967B CRC64;

Query Match 7.2%; Score 87.5; DB 11; Length 477;

Best Local Similarity 20.1%; Pred. No. 1.2;

Matches 47; Conservative 22; Mismatches 82; Indels 83; Gaps 8;

QY 19 LILSPCLNGTPDCYFSHPISNFEVKKRELTIDHLKDYPYAVNLQDEKCKALMSLF 78
 DB 233 LMERCPQEQFGDKYKLEPL-----PAEAVLKSSGSKNCIQRTAF 273
 QY 79 LAQRWIEQLKYAGSKMGTLEEDVNTETIHY--TSCFPOPLPECLRFVQTNISHLKDTC 136
 DB 274 LR-----SYLTSRSQSQSLDEGVLDHVMYMTSLYSPA-----VAVVCCYTC 316
 QY 137 TOLLALPKPCIGKACONFSRCL-----EVOCQDPSSTL-----PPRSP 174
 DB 317 PE---NPEVCGRRRLAVQEIILAAQGNLNAQODSNKVCSPQQLIFTRASSRSKSP 373
 QY 175 IALTELEPEPRROLLLLLPLTLVLLAAMGLRMQRRARRGELHPGVLP 228
 DB 374 AASRSTPAVTRKASLLPLQL-----RRSSVAPGVVVP 407
 RESULT 17
 Q9PKE2 PRELIMINARY; PRT; 1231 AA.
 AC Q9PKE2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DISEASE RESISTANCE PROTEIN RPS4.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLDMEIA;
 RX MEDLINE=96403884; Pubmed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI. sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and PAC clones."

RL DNA Res. 5:203-216(1998).
 DR EMBL: AB012240: BAB11396.1: -.
 DR InterPro: IPR000767: Disease_resist.
 DR InterPro: IPR001984: Lon_endopep.
 DR InterPro: IPR001611: LRR.
 DR InterPro: IPR002182: NB-ARC.
 DR InterPro: IPR000157: TIR.
 DR Pfam: PF00560: LRR; 8.
 DR Pfam: PF00931: NB-ARC; 1.
 DR Pfam: PF01582: TIR; 1.
 DR PRINTS: PRO0364: DISEASRESIST.
 DR PRINTS: PRO0830: ENDOLAPINASE.
 DR SMART: SM00253: TIR; 1.
 SQ SEQUENCE 1231 AA; 139730 MW; CC08AC0EDFEF885D4 CRC64;

Query Match 7.2%; Score 87.5; DB 10; Length 1231;
 Best Local Similarity 22.8%; Pred. No. 3.4; Mismatches 53; Conservative 32; Mismatches 74; Indels 73; Gaps 12;

QY 2 TVAPAMSPNSLLLL-----LLSPCLRGTPDCTFSFSPSSNFK----- 43
 DB 626 TELPPDYPNNLLDLRPYSNTITLWSCVKVAPNKKWDLSSNSLNSIMGLSEAPNLLR 685
 QY 44 -----VKFRELTDHLKDYPYVAVNLODEKCKALMSLELAORWIEOLKTAVAGSKMOT 97
 DB 686 LNEGCSLKELPDE-MKDMTNVFLNL---RGCTSLLS-----LPKITNSLKT 731
 QY 98 LLEVNTEHFVYNSC-----TFQPLPECLRFVQTN-----ISHL-----LKOTC 136
 DB 732 LI-----LSGCSFQFEVEYISHLSLYLNGTEINGLPPAIGNLRLFLNLKC-C 781
 QY 137 TOLIALKPCIG--KACQ--NFSRCLEVOCPDPSSTLLPPRSPIALEATELPE 184
 DB 782 KNIATLPDCLGELKLSLOELKLSRCKIKTFPDYAKMESLVLLDGTSIAE 833

RESULT 18
 Q9VF50 PRELIMINARY; PRT; 1256 AA.
 AC Q9VF50;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE CG18516 PROTEIN.
 GN CG18516.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Fodoris A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpow G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., Mcherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon R., Nussken D.R., Pacible J.M.,
 RA Palazon M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL Science 287:2185-2195(2000).
 CC 1-COFACITOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
 DR EMBL: AEO03709; AAF55210.1; -.
 DR FlyBase: FBgn0038350; CG18516.
 DR InterPro: IPR002888; 2FE-2S-BD.
 DR InterPro: IPR000564; 2FE2S_ferredoxin.
 DR InterPro: IPR000674; Aldxan_dh.C.
 DR InterPro: IPR002346; dehydrog_molyb.
 DR InterPro: IPR001041; Ferredoxin.
 DR Pfam: PF01315; Ald_xan_dh.C; 3.
 DR Pfam: PF02738; Ald_xan_dh.C; 2.
 DR Pfam: PF00941; FAD_binding_5; 1.
 DR Pfam: PF00111; fer2; 1.
 DR Pfam: PF01799; fer2.2; 1.
 DR ProDom: PD186071; 2Fe-2S-BD; 1.
 DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
 KW Iron-sulfur.
 SQ SEQUENCE 1256 AA; 138608 MW; A22459952D037420 CRC64;

Query Match 7.1%; Score 87; DB 5; Length 1256;
 Best Local Similarity 21.6%; Pred. No. 4; Mismatches 43; Conservative 28; Mismatches 56; Indels 72; Gaps 9;

QY 9 SPNSLLLLLLLSPLCRTPPCYFHSHP-----ISSNFKYKFEFLPD----- 51
 DB 650 SPSSNFKLM-----PSLK---DVFSSETPDTSRIIPLVLSIKLKEFSDKDPDLEVRGIFE 701
 QY 52 -----HLKDYPYVAVNLODEKCKALMSLELAORWIEOLKTAVAGSKMOTILEDVNTET 106
 DB 702 MGQYHFTMEPQTIIIPEDG-----LKVFSATQWIDQNGSVIARHLQKAKADVOLEV 755
 QY 107 H-----FVYSCTFQPLPECLRFVQTNISHLKDTCTQLALAKPCIGK- 148
 DB 756 RRLGSGYCKISRGNOVACAALAAHKLINRPVFOVS-----LESMDCNGKR 803
 QY 149 -ACQNFSCLEVOCPDPS 166
 DB 804 WACRS-----EYQCHWKTS 817
 RESULT 19
 Q91802 PRELIMINARY; PRT; 2111 AA.
 AC Q91802;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG1866 PROTEIN.
 GN KL-2 OR CG17866.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed-10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandlides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Ball J.F., Adiyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davernport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson A.,
 RA Merkulov G., Misha N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003219; AAG22465.1; -
 DR Flybase: FBgn0001313; K1-2.
 DR InterPro: IPR001901; SecE.
 DR PROSITE: PS01067; SecE_SPC61G; UNKNOWN_1.
 SQ SEQUENCE 2111 AA; 242787 MW; 00DZA0DB7A3D36B CRC64;

Query Match 7.1%; Score 86.5; DB 5; Length 2111;
 Best Local Similarity 21.1%; Pred. No. 8.1;
 Matches 58; Conservative 42; Mismatches 90; Indels 85; Gaps 10;

QY 11 NSLLLLLLLSPCLGTPDCYFSH-----SPISNFYKFR----- 47
 DB 989 NGVLLTTEALYSFILNVBD--FLHVALCFSPIGENFRSYROYRALLSSTTPMFRFWP 1046
 QY 48 -----ELTDHLKDYEVYAVN-LODEKHKAL--WSFLAQRWTEOLKTVAGSKMOTLL 99
 DB 1047 QEALLLEVASHFLGFLPLNVVSGKDEKRESLYVSTEAILQRODAYVFSYHSSVAKMS 1106
 QY 100 EDVNTET--HFVTS-----CTROPLEPCIRFVQTNISHLKTCQOLALK----- 143
 DB 1107 ENMYAEVKRYNYTSPNYIQLVSGFKLLKRRLEVSANRLRGLSKISFTEQKVSIM 1166
 QY 144 -----PCIGKACNFSRCLEVOQCQPSSTLLPSPRIAEATELPEPRROLLL 192
 DB 1167 SEELKASSEQVKILARECEDFISMIEIQ-----KSEATEQKEKYDAEAVL 1211
 QY 193 LLLPLPTLVLLAAAGLQRARRRGEELHPGVL 227
 DB 1212 IRDEITICELIATA-----RADLEEVMPM 1236

RESULT 20

Q9GPNB PRELIMINARY; PRT; 4167 AA.
 ID Q9GPNB;
 AC Q9GPNB;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN 1-BETA DYNEIN (FRAGMENT).
 GN KL-2 OR CG17866.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20542110; PubMed-11069293;
 RA Carvalho A.B., Lazaro B.P., Clark A.G.;
 RT "Chromosomal fertility factors Kl-2 and Kl-3 of *Drosophila*
 RT melanogaster encode dynein heavy chain polypeptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13239-13244(2000).
 DR EMBL: AF313479; AAG29345.1; -
 DR Flybase: FBgn0001313; K1-2.
 DR InterPro: IPR003593; AAA.
 DR SMART: SM00382; AAA; 2.
 DR ATP-Binding.
 KW NON_TER
 FT NON_TER
 SQ SEQUENCE 4167 AA; 483035 MW; 5FA8BC54B67CC205 CRC64;

Query Match 7.1%; Score 86.5; DB 5; Length 4167;
 Best Local Similarity 21.1%; Pred. No. 18;
 Matches 58; Conservative 42; Mismatches 90; Indels 85; Gaps 10;

QY 11 NSLLLLLLLSPCLGTPDCYFSH-----SPISNFYKFR----- 47
 DB 2592 NGVLLTTEALYSFILNVBD--FLHVALCFSPIGENFRSYROYRALLSSTTPMFRFWP 2649
 QY 48 -----ELTDHLKDYEVYAVN-LODEKHKAL--WSFLAQRWTEOLKTVAGSKMOTLL 99
 DB 2650 QEALLLEVASHFLGFLPLNVVSGKDEKRESLYVSTEAILQRODAYVFSYHSSVAKMS 2709
 QY 100 EDVNTET--HFVTS-----CTROPLEPCIRFVQTNISHLKTCQOLALK----- 143
 DB 2710 ENMYAEVKRYNYTSPNYIQLVSGFKLLKRRLEVSANRLRGLSKISFTEQKVSIM 2769
 QY 144 -----PCIGKACNFSRCLEVOQCQPSSTLLPSPRIAEATELPEPRROLLL 192
 DB 2770 SEELKASSEQVKILARECEDFISMIEIQ-----KSEATEQKEKYDAEAVL 2814
 QY 193 LLLPLPTLVLLAAAGLQRARRRGEELHPGVL 227
 DB 2815 IRDEITICELIATA-----RADLEEVMPM 2839

RESULT 21

Q96164 PRELIMINARY; PRT; 962 AA.
 ID Q96164;
 AC Q96164;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE SERA ANTIGEN/PAPAIN-LIKE PROTEASE WITH ACTIVE SER.
 GN PEB0345C.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed-9804551;
 RA Gardner M.J., Tetteilin H., Carucci D.J., Cummings L.M., Aravind L.,

RA Koonin E.V., Shalloom S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum";
 RL Science 282:1126-1132(1998).
 DR EMBL; AE001388; AAC71858.1; -.
 DR MEROPS; C01.UNA; -.
 DR InterPro: IPR000668; Peptidase.C1.
 DR InterPro: IPR000169; Thiolprol.act.site.
 DR Pfam: PF00112; Peptidase.C1; 1.
 DR PROSITE: PS00640; TRITOL_PROTEASE_ASN; 1.
 KW Hydrolase; Protease; Thiol protease.
 SQ SEQUENCE 962 AA; 108680 MW; BF7659CC46D39495 CRC64;

Query Match 7.0%; Score 86; DB 5; Length 962;
 Best Local Similarity 20.9%; Pred. No. 3.7;
 Matches 31; Conservative 28; Mismatches 39; Indels 50; Gaps 7;

QY 8 WSPNSLLILLLLSPCLRGTPDCYFSPSSNF-----KVFRELTDHL----- 53
 DB 422 WMKNTKIGLL-----PQLSYDLTYKNNFTFTQNSQNTYVDRKLYCNHEYC 470
 QY 54 --LKDYPTVYVA-VNLODEKHKALMSLFLAQRNIEOLKTAVGSKMOTLLEDVNTFHEVT 110
 DB 471 NRIKDHNNICISKINVEDOKKALMSA-FASKYHLLETIKCMKG-----YEPLNAYVLYVT 523
 QY 111 SCTGQPLPECLRPVGTNISHLKDCTQ 138
 DB 524 NC-----LKNKNKDVCTE 536

RESULT 22
 ID 017726 PRELIMINARY; PRT; 181 AA.
 AC 017726;
 DT 01-JUN-1998 (TrEMBLrel. 05, Created)
 DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE D1086.1 PROTEIN.
 GN D1086.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN RABBITIDAE; Peleodermidae; Caenorhabditis.
 RA Snye R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RP MEDLINE=99069613; PubMed=9851916;
 RX SEQUENCE FROM N.A.
 RT none;
 RT "genome sequence of the nematode C. elegans: A platform for
 RT investigating biology";
 RL Science 282:2012-2018(1998).
 RL EMBL; Z81491; CAB04019.1; -.
 DR InterPro: IPR002542; DUF19.
 DR Pfam: PF01579; DUF19; 1.
 SQ SEQUENCE 181 AA; 20198 MW; 80128F93F6A4E822 CRC64;

Query Match 7.0%; Score 85; DB 5; Length 181;
 Best Local Similarity 23.5%; Pred. NO. 0.69;
 Matches 39; Conservative 24; Mismatches 59; Indels 44; Gaps 8;

QY 13 SLLILLLLSPCLRGTPDCYFSPSSNFVKFRELTDHLKD-----PPVTVAVNLQD 67
 DB 8 TILPELFLSKAENSPDSCSKDIDQIVTCRPLAKLIDKKKPLNSGPFVETLN-KM 66
 QY 68 EKHCKALMSLFLAQRNIEOLKTAVGSKMOTLLEDVNTFHEVTSC---TFQPLD----- 118

DB 67 SGICK-----EAMSCVSPAKCAPATEKMS---KFAIMTKTIDFMSGPYACAA 111
 QY 119 -----ECLRFVGTNISHLKD-TCYQALLAKRCI-----GKAC 150
 DB 112 KTKASNDKTECVQWYFSDKSRMSTDQKCAQFKAKKOCIEKDFGKAC 157

RESULT 23
 ID 006521 PRELIMINARY; PRT; 1305 AA.
 AC 006521;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AGGREGATION SUBSTANCE.
 GN ASH701.
 OS Enterococcus faecium (Streptococcus faecium).
 OG Plasmid PHK701.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R7;
 RX MEDLINE=96257186; PubMed=8675038;
 RA Heaton M.P., Discotto L.F., Pucci M.J., Handwerker S.;
 RT "Mobilization of vancomycin resistance by transposon-mediated fusion
 RT of a VanA plasmid with an Enterococcus faecium sex pheromone-response
 RT plasmid";
 RL Gene 171:9-17(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R7;
 RA Heaton M.P., Handwerker S.;
 RT "Aggregation substance gene from Enterococcus faecium R7 PHK701.";
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U91527; AAB58159.1; -.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000566; Lipoclin_cyFABP.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 KW PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 SQ SEQUENCE 1305 AA; 142496 MW; CBC342350A6F8A1 CRC64;

Query Match 7.0%; Score 85; DB 2; Length 1305;
 Best Local Similarity 21.1%; Pred. NO. 6.7;
 Matches 43; Conservative 29; Mismatches 60; Indels 72; Gaps 9;

QY 38 ISSNFVKFRELTDHLKDYPVTVAVNLQDEKHKALMSLFLAQRNIEOLKTAVGSKMOT 97
 DB 1151 ISKLTMTPEQGVAVITSAQFLDAMNLKENKHVHSMKAFIG---VERI--AAGNYVNT 1205
 QY 98 LLEDVNTFHEVYVSTGFPDLPECLRFVQTN--ISHLKDTCYQALLAKPCGKACQNSR 155
 DB 1206 IESEFNNET-----IKNTVVTHTPE-----RP----- 1228
 QY 156 CLEVQCQPDSSSTLLP-----PRSPALE-----ATELPAPRRQILLILL 196
 DB 1229 ----QTPPEKTVIVSTPTAPKTPQVPPVQAPEPLVEKASVYPLLPOTGEGNILLIVA 1284

RESULT 24
 ID 09MBF8 PRELIMINARY; PRT; 4513 AA.
 AC 09MBF8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE 1 BETA DYNEIN HEAVY CHAIN.
 GN DYC10.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21 GR;
 RX MEDLINE=20346958; PubMed=10888669;
 RA Bertone C.A., Myster S.H., Bower R., O'Toole E.T., Porter M.E.;
 RT "Insights into the structural organization of the 11 inner arm dynein
 RT from a domain analysis of the 1 beta dynein heavy chain."
 RL Mol. Biol. Cell 11:2297-2313(2000).
 DR EMBL; AJ242523; CAB99316.1;
 DR EMBL; AJ242524; CAB99316.1; JOINED.
 DR EMBL; AJ242525; CAB99316.1; JOINED.
 DR InterPro; IPR004273; Dynein_heavy.
 DR InterPro; IPR000005; HTHArc.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF03028; Dynein_heavy; 1.
 DR PROSITE; PS00041; HTH_ARC_FAMILY_1; UNKNOWN_1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 SQ SEQUENCE 4513 AA; 510655 MW; F2A3E10767FD6719 CRC64;

Query Match 7.0%; Score 85; DB 10; Length 4513;
 Best Local Similarity 24.1%; Pred. No. 28;
 Matches 49; Conservative 29; Mismatches 71; Indels 54; Gaps 10;

QY 47 RELTDLKLD-----YPTVAVNIQDEKCKALMSLFLAQRIEQLKTVAGSKMOTLE 100
 Db 796 RSISELVLDVEKKIYQHAERANLOESHAKIKDRLVSA---VDEIRDIMAS-IHVEE 851
 QY 101 DVNTEIHVFVSCFQPLPECLRFVQTNISHLKDTQTQLALKPCIGACONFSRCLEVQ 160
 Db 852 QDSEEVQ-----REWVRFTQ-KVDRKLED-----ALRHVKKSLQELSRLL--- 891
 QY 161 CQPDSSTLPP--RSPIALEATELEPPRP-----RQLLLILLPLTLVLLA 205
 Db 892 -NGDNKTEVPFIHVTVLETRNRELRTIQALFTINSVARNLLIVLSVPRV----- 945
 QY 206 AAMGLRWORARRRGELHPGVPLP 228
 Db 946 ---ALQLTKQRDMEDAGLPLP 965

RESULT 25
 Q96AY5 PRELIMINARY; PRT; 364 AA.
 AC Q96AY5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE HYPOHETICAL 40.2 KDA PROTEIN (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eulheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA, AND CHORIOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016451; AHH16451.1; -.
 KW Hypothetical protein.
 FT NO_TER 1
 SQ SEQUENCE 364 AA; 40210 MW; A3D54D967D67FD30 CRC64;

Query Match 6.9%; Score 84.5; DB 4; Length 364;

Best Local Similarity 21.9%; Pred. No. 1.7;
 Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;
 QY 40 SNPKVRFRELTDLKLDYPTVAVNIQDEKCKALMSLFLAQRIEQLKTVAGSK----- 94
 Db 35 SDNKVYHRSFCEANKKPKFIRMCNIOCTH-----PLWVAEEMERCTYCGSSGYOLRT 89
 QY 95 ---MOTLEDVNTETIHFV-----TSCTFQPLP-----ECLRFV--OTNISH 130
 Db 90 VRCLOPLDGTIRSVASKCKMGDRPESRRCNRYPCPAQMKKTGPMSECSYTCGEETEVQ 149
 QY 131 LL-----KDTCTQLALKPCIGKAC-----QNTSRCLFVQC 161
 Db 150 VLRAGDHCDGKPPSVRACQLPCNDPCLGDKSIFCQMEVILARYCSIPYKRLCCESC 209
 QY 162 QPDSSTLPPRSPIALEATEL-----PEPRRQLLLILLPL 198
 Db 210 SKRSSR-LPP--PYLLEAETHDVIYSNPSDLPRSLVMPSTLVP 250

Search completed: August 6, 2002, 09:45:52
 Job time: 408 sec

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:02 ; Search time 53.63 Seconds

(without alignments)
478.427 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223

Scoring table: BLOSUM62

searched: 747574 seqs, 111073796 residues

local number of hits satisfying chosen parameters: 747574

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1980.DAT *
2:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1981.DAT *
3:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1982.DAT *
4:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1983.DAT *
5:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1984.DAT *
6:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1985.DAT *
7:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1986.DAT *
8:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1987.DAT *
9:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1988.DAT *
10:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1989.DAT *
11:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1990.DAT *
12:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1991.DAT *
13:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1992.DAT *
14:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1993.DAT *
15:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1994.DAT *
16:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1995.DAT *
17:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1996.DAT *
18:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1997.DAT *
19:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1998.DAT *
20:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA1999.DAT *
21:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA2000.DAT *
22:	/SID5/gcgdata/geneseq/geneseqp_emb1/AA2001.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1233	100.0	231	16	AA067540	Mouse Flt-3 ligand
2	1223	100.0	231	20	AA067768	Mouse Flt-3 ligand
3	1223	100.0	231	20	AA067186	Murine Flt3-ligand
4	1212.5	99.1	232	16	AA066177	Mouse Flt-3 ligand
5	1208.5	98.8	232	22	AA020189	Mouse MCT10/1118
6	1006	82.3	288	22	AA002129	Mouse Flt-3 ligand
7	1004	82.1	189	22	AA020187	Flt-3 ligand (FL)
8	879	71.9	172	22	AA020191	Mouse Flt-3 ligand
9	879	71.9	220	22	AA020188	Mouse Flt-3 ligand
10	879	71.9	220	22	AA020190	Mouse Flt-3 ligand
11	774	63.3	294	21	AA058204	Canine Flt-3 ligand

12	772.5	63.2	235	16	AAR66175	Human S66/S109 F1T3
13	772.5	63.2	235	16	AAR620134	Human Flt-3 ligand
14	768.5	62.8	235	16	AAR67341	Human Flt-3 ligand
15	768.5	62.8	235	20	AAAG6759	Human Flt-3 ligand
16	768.5	62.8	235	21	AAAG69719	Human Flt3-Ligand
17	768.5	62.8	235	22	AAAB20192	Full length wild t
18	761	62.2	291	21	AAAG58210	Human Flt-3 ligand
19	692	56.6	212	21	AAAG59721	Pellicle Flt-3 ligand
20	687	56.2	209	21	AAAG59724	Human Flt-3 mutetin
21	686	56.1	209	19	AAAG59007	Human Flt-3 mutetin
22	686	56.1	209	21	AAAG59720	Human Flt-3 recept
23	686	56.1	209	21	AAAG69723	Human wild type h
24	685	56.0	209	21	AAAG69725	Mature Flt-3 recept
25	685	55.8	209	21	AAAG59725	Human Flt-3 mutetin
26	682	55.8	209	21	AAAG59726	Human Flt-3 mutetin
27	682	55.8	209	21	AAAG59727	Human Flt-3 mutetin
28	682	55.8	209	21	AAAG59729	Human Flt-3 mutetin
29	680	55.6	209	21	AAAG69722	Human Flt-3 mutetin
30	679.5	55.6	268	21	AAAG58206	Human Flt-3 mutetin
31	679	55.5	209	21	AAAG59728	Canine mature Flt-
32	666.5	54.6	276	21	AAAG59728	Canine Flt-3 mutetin
33	666.5	54.3	265	21	AAAG58207	Canine Flt-3 ligand
34	663.5	54.3	185	22	AAAG58211	Pellicle mature Flt-
35	594.5	48.6	178	22	AAAB20195	Human Flt-3 ligand
36	573.5	46.9	250	21	AAAB20193	Human Flt-3 ligand
37	548.5	44.8	377	19	AAAG8208	Canine mature Flt-
38	545	44.6	349	19	AAAG8124	Chimeric recept
39	545	44.6	349	19	AAAG83286	Human Flt3 ligand
40	545	44.6	523	19	AAAG83286	Human Flt3 ligand
41	542.5	44.4	334	19	AAAG78005	Human Flt3 ligand
42	542.5	44.4	334	19	AAAG78005	Human Flt3 ligand
43	541	44.2	101	16	AAAG78280	Human Flt-3 ligand
44	541	44.2	140	19	AAAG78281	G-CSF-Flt-3 ligand
45	541	44.2	140	19	AAAG7911	Flt3 ligand
46	541	44.2	140	19	AAAG69035	Human Flt3 ligand
47	541	44.2	143	19	AAAG79216	Human Flt-3 recept
48	541	44.2	144	19	AAAG69050	Human Flt-3 recept
49	541	44.2	144	19	AAAG79298	Flt3 ligand
50	541	44.2	150	19	AAAG69052	Human Flt-3 recept
					AAAG77930	Flt3 ligand

ALIGNMENTS

RESULT	1
AA67540	
ID	AA67540 standard; Protein; 231 AA.
XX	
AC	AA67540;
XX	
DT	05-AUG-1995 (first entry)
XX	
DE	Mouse flt-3 ligand.
XX	
XX	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy
OS	Mus sp.
XX	
EH	Key
FT	Peptide
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
XX	
PN	EP627487-A.
XX	
PD	07-DEC-1994.
XX	
XX	19-MAY-1994; 94EP-0303575.

XX 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMMUNEX CORP.
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB; AA079076.
 XX
 PR Isolated ligands for flt 3 receptors - useful for treating
 PR anaemia, AIDS and various cancers
 PR
 PS Disclosure: Page 25-27; 33pp; English.
 XX
 CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a
 CC cDNA library of T-cell line P7B-0.344 in CY-1/EBNA-1 cells
 CC using a slide autoradiography method. Flt3-L stimulates
 CC production of progenitor and stem cells, and can be used e.g.
 CC in gene therapy protocols.
 CC
 XX
 SQ Sequence 231 AA;

Query Match 100.0%; Score 1223; DB 16; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPNSLLILLLISPCLRGTPDCYFSHSPISSNKKVRFELTDHLKDYPT 60
 DB 1 mtvalapawspnsllililispclirgtpdcyfsnspisnkkvrfeltdhlkdypt 60
 QY 61 VAVNIDDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLEDVNTTEHFVTSCTFQPLPEC 120
 DB 61 vavniddekhckalmslflaqrwieqlktvagskmqtlledvntelhfvtscctfqp1pec 120
 QY 121 LRFVQTNISHLKRTCTQLALAKPCIGKACONFSRCLEVQCCOPDSSSTLLPPRSPIALEAT 180
 DB 121 lrfvqtnishlkrctqqlalpkpcigkacqnfsrcleevqcpdssstllpprspialeat 180
 QY 181 ELPEPRPROLILLLPLTLVLLAAAGLIRWQARRRGELHPGVLPSPHP 231
 DB 181 elpeprprqlilililpltlvllaaaglrwqarrrrgelhpgvlpshp 231

RESULT 2
 AAW67768
 ID AAW67768 standard; Protein; 231 AA.
 XX
 AC AAW67768;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Murine flt3-ligand.
 XX
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 OS
 XX Mus sp.
 XX
 PN W09857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98MO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.

XX
 PA (IMMUNEX CORP.
 XX
 PI Abbott NM, Mowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB; AAW81505.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 PS
 XX
 PS Claim 1: Page 12; 25pp; English.
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents murine flt3-L.
 XX
 SQ Sequence 231 AA;

Query Match 100.0%; Score 1223; DB 20; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPNSLLILLLISPCLRGTPDCYFSHSPISSNKKVRFELTDHLKDYPT 60
 DB 1 mtvalapawspnsllililispclirgtpdcyfsnspisnkkvrfeltdhlkdypt 60
 QY 61 VAVNIDDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLEDVNTTEHFVTSCTFQPLPEC 120
 DB 61 vavniddekhckalmslflaqrwieqlktvagskmqtlledvntelhfvtscctfqp1pec 120
 QY 121 LRFVQTNISHLKRTCTQLALAKPCIGKACONFSRCLEVQCCOPDSSSTLLPPRSPIALEAT 180
 DB 121 lrfvqtnishlkrctqqlalpkpcigkacqnfsrcleevqcpdssstllpprspialeat 180
 QY 181 ELPEPRPROLILLLPLTLVLLAAAGLIRWQARRRGELHPGVLPSPHP 231
 DB 181 elpeprprqlilililpltlvllaaaglrwqarrrrgelhpgvlpshp 231

RESULT 3
 AAB20186
 ID AAB20186 standard; Protein; 231 AA.
 XX
 AC AAB20186;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mouse Flt-3 ligand.
 XX
 KW Flt-3 ligand; fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 OS
 XX Mus musculus.
 XX
 FH Key
 FT Peptide 1..27
 FT Protein /label- Signal_peptide
 FT 28..231
 FT /label- Mature_protein

Query Match	Best Local Similarity	100.0%;	Score 1223;	DB 22;	Length 231;
Matches 231;	Conservative	0;	Mismatches	0;	Indels
					Gaps
QY	1	MTVLAPANSNSLLILLILSLSPCLRGRPDCTFFSSPISSNFKVFRRLTDLKLDYPT	60		
Db	1	mtvlapawspnslllllllllspclrtpdcyfcfsspslntkfvfreltdhllkdypt	60		
OY	61	VAVNLDKRCFKALMSFLAORMIOLKTVGSKMOTLLEDVNTFHHPTSCQPLRPEC	120		
Db	61	vavnnqdekhckalvslflaqwsiqkltvagxmqctllledvntelhtvtsctfiprpec	120		
OY	121	LRFVQTNISHLKDNCTDILLKPCIGKACQNFSSCLLEVOCQPDSSSTLLPPRSPIALEAT	180		
Db	121	lrfvgttnslhllktdctqllalkpqlgkacqfscrlwgcqpdssstllpprsplaleat	180		
OY	181	ELPFRPRQLLLILLPLTLVLAAAGLKRQARRRGEELHPVLPSPHP	231		

```

Db      101 elpeprpqrllllllplclvl1aaawglwqrrrrgelhpvlpfshp 231
        RESULT      4
        ID          AAR66177
        AC          AAR66177 standard; Peptide; 232 AA.
        XX
        XX          AAR66177;
        DE          10-AUG-1995 (first entry)
        OS          Homo sapiens.
        KW          Flt3 ligand; tyrosine kinase receptor ligand.
        XX
        XX          Mouse MoT110/T118 Flt3 ligand peptide fragment.
        PD          24-NOV-1994.
        PE          18-MAY-1994; 94MO-US05150.
        PF          19-MAY-1993; 93US-0065231.
        PR          07-JUL-1993; 93US-0089263.
        PR          16-JUL-1993; 93US-0092549.
        PR          13-AUG-1993; 93US-0106340.
        PR          24-AUG-1993; 93US-0112391.
        PR          19-NOV-1993; 93US-0155111.
        PR          03-DEC-1993; 93US-0162413.
        XX
        PA          (INRM ) INST NAT SANTE & RECH MEDICALE.
        PA          (SCHE ) SCHERING CORP.
        XX
        PI          Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
        DR          WPI; 1995-006787/01.
        DR          N-PSDB; AAQ79464.
        XX
        PT          New ligand for the Flt3 tyrosine kinase receptor - and related
        PT          nucleic acid, vectors, host cells and antibodies, useful for
        PT          treating abnormal cell physiology and proliferation, e.g. cancer,
        PT          also for diagnosis and drug screening
        XX
        PS          Claim 11: page 79-80; 90pp; English.
        CC
        CC          A cDNA library from the human stromal cell line 29SV48, in
        CC          pME185, was screened with an 800 bp fragment derived from
        CC          mouse clone T118. This fragment encompasses the coding region
        CC          conserved between two mouse clones, T118 and T110. Approx. 20
        CC          positive clones were selected and partially sequenced. Two
        CC          clones, S86 and S109, were found to be approx. 75% homologous
        CC          to the mouse clones over the first 163 AAs. Clone S86 continued
        CC          to show homology to T110 until the stop codon, although to a
        CC          lesser degree, for an overall homology of 66%. Clones T118 and
        CC          S109 do not show homology to each other or to the other clones
        CC          after mouse residue 163 (human residue 160). An additiona mouse
        CC          clone designated MB8 has a 29 AA insert at the junction between
        CC          the common and divergent portions of the mouse ligand.
        CC
        SS          Sequence      232 AA;
        OY
        OY          Query Match      99.1%; Score 1212.5; DB 16; Length 232;
        Db      Best Local Similarity 99.6%; Pred.No. 5e-114;
        Mch     Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1.
        OY          1 MTVLAPAMSNSSLILLLLSPLCRGPRDCYFSSPISNFKYKPRELNDHLTKPYPT 60
        Db      1 mtvlapawspnslllllllllspcrlrgpdccyfnspisnfxkfkrelcdhlkkdypvt 60
        OY          61 VAVNVLOEKCKALMSLFIAQRNIQLDKTVAGSKMOTLLEDVNTEIHFRVTSCTFPDLPQC 120

```

Db 61 vavnlqdekhnckalwslflagrwleqlktvagskmgllledvntelhfvtscftqplpec 120
QY 121 LRFVQTNIHSLKDTCTQLLAKPCIGKACQNFSCLEVOQCPDSSSTLLPPRSIALPEAT 180
Db 121 lrfvqtnishlkdctctqlgkpcigkacqnfsclevoqcpdssstllpprsialeat 180
QY 181 ELPEPRPRQ-LLLLLLLPLFTVLVLAAMGLRMORARRRGELHPGVPPLPSHP 231
Db 181 elpeprprqlllllllllplctivllaawglrwqrrrrgelhpgvpplpsnp 232

RESULT 5
AAB20189
ID AAB20189 standard; Protein: 232 AA.
XX AAB20189;
XX 14-MAY-2001 (first entry)
XX Mouse Flt-3 ligand.
XX
XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= Signal_peptide
FT 28..232
FT /label= Mature_protein
FT 28..188
FT /label= Extracellular_domain
FT 189..212
FT /label= Transmembrane_domain
FT 213..232
FT Domain
FT /label= Cytoplasmic_domain
XX
XX W0200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VIC-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI; 2001-123319/13.
XX N-PSDB; AAF30307.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 125-126; 149pp; English.
XX
XX The present sequence is that of mouse Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present sequence of the mature
CC polypeptide. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for

CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.
XX
SQ Sequence 232 AA:
XX
XX Query Match 98.8%; Score 1208.5; DB 22; Length 232;
XX Best Local Similarity 99.1%; Pred. No. 1.3e-113;
XX Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MVLAPAMSPNSSLILLILLSPCLRGTPDCYFHSPISSNFKVKFRELTHLKDHYVT 60
Db 1 mtvlapawspnsalllllllllspclrgtpdcyfhspissnfkvfreldhllkdypt 60
QY 61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
Db 61 vavnlqdekhnckalwslflagrwleqlktvagskmgllledvntelhfvtscftqplpec 120
QY 121 LRFVQTNIHSLKDTCTQLLAKPCIGKACQNFSCLEVOQCPDSSSTLLPPRSIALPEAT 180
Db 121 lrfvqtnishlkdctctqlgkpcigkacqnfsclevoqcpdssstllpprsialeat 180
QY 181 ELPEPRPRQ-LLLLLLLPLFTVLVLAAMGLRMORARRRGELHPGVPPLPSHP 231
Db 181 elpeprprqlllllllllplctivllaawglrwqrrrrgelhpgvpplpsnp 232

RESULT 6
AAU02129
ID AAU02129 standard; Protein: 288 AA.
XX AAU02129;
XX
XX 29-AUG-2001 (first entry)
XX
XX Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.
XX
XX Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A;
KW ETA dII; antigenic; immunogenic; cytotoxic T cell response; tumour;
KW vaccine; immunotherapy.
XX
XX OS Unidentified.
XX
XX W0200129233-A2.
XX
XX 26-APR-2001.
XX
XX 20-OCT-2000; 2000WO-US41422.
XX
XX 20-OCT-1999; 99US-0421608.
XX PR 09-FEB-2000; 2000US-0501097.
XX
XX (UYJO) UNTV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Wu T, Hung C;
XX
XX WPI; 2001-290921/30.
XX
XX New chimeric polypeptide, useful as anti-tumour vaccines, comprises
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and
PT antigenic polypeptide -
XX
XX Claim 9; Fig 19; 110pp; English.
XX

XX 14-MAY-2001 (first entry)
XX
XX Mouse Flt-3 ligand.
DE
XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW immunotherapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Signal_peptide
FT 28..172
FT Protein /label= Mature_protein
XX
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI: 2001-123319/13.
XX
XX N-PSDB; AAF30309.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Claim 2; Page 130; 149pp; English.
XX
XX The present sequence is that of mouse Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present sequence or the mature
CC polypeptide. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Anjeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.
XX
XX Sequence 172 AA;
SQ

Query Match 71.9%; Score 879; DB 22; Length 172;
Best Local Similarity 98.2%; Pred. No. 1.4e-80;
Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLLILLILSPCLRTGTPCYFSHSPISSEFKVKKFRELTHLTKYPT 60
Db 1 mtvalapwspnslllllllllspclrtgtpcyfshspisnfvkfkrelthllkkypt 60
QY 61 VAVNLDEKHCKALWSLFLAQRWIEOLKTIVAGSKMOTLLEDVNTETIHFTVSTCFOPLPBC 120

Db 61 vavnlqdekhckalwsiflaqrwieqlktvagskmgltlledvnteihftvstctfpipcc 120
QY 121 LRFVQNTSHLKKQCTQLAARPCIGKACQNFSCLEVCQOPDSSRL 168
Db 121 lrfvqntshllkktctqlaalkpckigkacqnfsclevcqopdssrl 168
RESULT 9
AAB20188
ID AAB20188 standard; Protein: 220 AA.
XX
XX AAB20188;
AC
XX
XX 14-MAY-2001 (first entry)
DE
XX
XX Mouse Flt-3 ligand.
XX
XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW immunotherapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= Signal_peptide
FT 28..220
FT Protein /label= Mature_protein
XX
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI: 2001-123319/13.
XX
XX N-PSDB; AAF30306.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. Rheumatoid arthritis) -
XX
XX Claim 2; Page 123-124; 149pp; English.
XX
XX The present sequence is that of mouse Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present sequence or the mature
CC polypeptide. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Anjeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

```

XX      XX      Sequence      220 AA;
SQ      Query Match
          71.9%; Score 879; DB 22; Length 220;
          Best Local Similarity 82.3%; Pred. No. 2e-80;
          Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHPISNFYKFKRELTDHLKDPYPT 60
          1 mcvlapawspsslllllllspclrgtpdcyfsfshpsisnfkvtreltdhlkdpvt 60
          Db
          61 VAVNIQDEKHCKALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPIPEC 120
          61 vavniqdekhckalmslflaqrmieqlktvagskmgctllledvntelhfvtscctfqpipcc 120
          Db
          121 LRFVQNTISHLKDFCTQLALKPCIGKACQNFSCLEVOCPDPSSTLLPPRS----PIA 176
          121 lrfvqntishlkkdctcqlalpkpcigkacqnfsrclevqcpqng---gpraqhngatr 177
          Db
          177 LEATELPEPRPRLDLL-----LILLPLTLVLAA 206
          178 ltatalltvcpglllpivgtshmfllpyflsfllss 212

RESULT 10
AAB20190
ID      AAB20190 standard; Protein; 220 AA.
XX
AC      AAB20190;
XX
DT      14-MAY-2001 (first entry)
XX
DE      Mouse Flt-3 ligand.
XX
KW      Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KM      immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW      lymphoma; autoimmune disease; infection; gene therapy.
XX
OS      Mus musculus.
XX
FH      Key
FT      Peptide      1..27      Location/Qualifiers
FT      Protein      /label= Signal_peptide
FT      Protein      /label= Mature_protein
XX
PN      WO200109303-A2.
XX
PD      08-FEB-2001.
XX
PF      31-JUL-2000; 2000WO-US20679.
XX
PR      30-JUL-1999; 99US-0146170.
XX
PA      (VICA-) VICAL INC.
XX
PI      Hermanson GG;
XX
DR      WPI: 2001-123319/13.
DR      N-PSDB; AAF30308.
XX
PT      Immunogenic compositions comprising Flt-3 ligand encoding
PT      polynucleotide and one or more antigen, or cytokine encoding
PT      polynucleotides, useful for suppressing tumour growth and for treating
PT      autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS      Claim 2; Page 128; 149pp; English.
XX
CC      The present sequence is that of mouse Fms-like tyrosine kinase
CC      (Flt-3 ligand). The invention is directed to enhancing the
CC      immune response of a vertebrate to an antigen or a cytokine by
CC      administering in vivo, into a tissue of a vertebrate, a Flt-3

```

```

CC      ligand-encoding polynucleotide, and 1 or more antigen- or
CC      cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC      polynucleotide may encode the present sequence or the mature
CC      polypeptide. The polynucleotides are incorporated into
CC      the cells of the vertebrate in vivo, and a prophylactically or
CC      therapeutically effective amount of Flt-3 ligand and 1 or more
CC      antigens or cytokines is produced in vivo. Pharmaceutical
CC      compositions comprising the polynucleotides are useful for
CC      suppressing tumour growth in a mammal. The tumour is melanoma,
CC      glioma or lymphoma, particularly B-cell lymphoma. They can also
CC      be used for the prophylactic and/or therapeutic treatment of:
CC      (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC      and C in humans), parasitic (e.g. malaria) and fungal infections;
CC      (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC      osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC      Various other examples of these diseases are given in the
CC      specification.
XX
SQ      Sequence      220 AA;

Query Match
          71.9%; Score 879; DB 22; Length 220;
          Best Local Similarity 82.3%; Pred. No. 2e-80;
          Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHPISNFYKFKRELTDHLKDPYPT 60
          1 mcvlapawspsslllllllspclrgtpdcyfsfshpsisnfkvtreltdhlkdpvt 60
          Db
          61 VAVNIQDEKHCKALMSLFLAQRMIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPIPEC 120
          61 vavniqdekhckalmslflaqrmieqlktvagskmgctllledvntelhfvtscctfqpipcc 120
          Db
          121 LRFVQNTISHLKDFCTQLALKPCIGKACQNFSCLEVOCPDPSSTLLPPRS----PIA 176
          121 lrfvqntishlkkdctcqlalpkpcigkacqnfsrclevqcpqng---gpraqhngatr 177
          Db
          177 LEATELPEPRPRLDLL-----LILLPLTLVLAA 206
          178 ltatalltvcpglllpivgtshmfllpyflsfllss 212

RESULT 11
AAV58204
ID      AAV58204 standard; Protein; 294 AA.
XX
AC      AAV58204;
XX
DT      14-MAR-2000 (first entry)
XX
DE      Canine Flt-3 ligand.
XX
KW      Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
KW      immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS      Canis familiaris.
XX
PN      WO9961618-A2.
XX
PD      02-DEC-1999.
XX
PF      28-MAY-1999; 99WO-US11942.
XX
PR      29-MAY-1998; 98US-0087306.
XX
PA      (HESK-) HESKA CORP.
XX
PI      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR      WPI: 2000-072623/06.
DR      N-PSDB: AA255487, AA255488, AA255489, AA255490.
XX
PT      Nucleic acids encoding immunoregulatory proteins from cats or dogs,

```


XX	Key	Location/Qualifiers
FH	Peptide	1..26
FT		/label= Signal_peptide
FT	Protein	27..235
FT		/label= Mature_protein
FT	Domain	27..182
FT		/label= Extracellular_domain
FT	Domain	183..205
FT		/label= Transmembrane_domain
FT	Domain	206..235
FT		/label= Cytoplasmic_domain
XX		
FN	WO200109303-A2.	
PD	08-FEB-2001.	
XX		
PF	31-JUL-2000; 2000WO-US0679.	
XX		
PR	30-JUL-1999; 99US-0146170.	
XX		
PA	(VICCA-) VICAL INC.	
XX		
P1	Hermanson GG;	
XX		
DR	WPI; 2001-123319/13.	
DR	N-PSDB; AAF30312.	
XX		
PT	Immunogenic compositions comprising Flt-3 ligand encoding	
PT	polynucleotide and one or more antigen, or cytokine encoding	
PT	polynucleotides, useful for suppressing tumour growth and for treating	
PT	autoimmune diseases (e.g. rheumatoid arthritis) -	
XX		
PS	Claim 2; Page 137-138; 149pp; English.	
XX		
CC	The present sequence is that of human Fms-like tyrosine kinase	
CC	(Flt-3 ligand). The invention is directed to enhancing the	
CC	immune response of a vertebrate to an antigen or a cytokine by	
CC	administering in vivo, into a tissue of a vertebrate, a Flt-3	
CC	ligand-encoding polynucleotide, and 1 or more antigen- or	
CC	cytokine-encoding polynucleotides. The Flt-3 ligand-encoding	
CC	polynucleotide may encode the present full-length human Flt-3	
CC	ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235	
CC	of the Flt-3 ligand. The polynucleotides are incorporated into	
CC	the cells of the vertebrate in vivo, and a prophylactically or	
CC	therapeutically effective amount of Flt-3 ligand and 1 or more	
CC	antigens or cytokines is produced in vivo. Pharmaceutical	
CC	compositions comprising the polynucleotides are useful for	
CC	suppressing tumour growth in a mammal. The tumour is melanoma,	
CC	glioma or lymphoma, particularly B-cell lymphoma. They can also	
CC	be used for the prophylactic and/or therapeutic treatment of:	
CC	(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B	
CC	and C in humans), parasitic (e.g. malaria) and fungal infections;	
CC	(b) autoimmune diseases (e.g. rheumatoid arthritis and	
CC	osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.	
CC	Various other examples of these diseases are given in the	
CC	specification.	
XX		
Sequence	235 AA;	
XX		

[illegible]

ID	AA067541	standard; Protein; 235 AA.
XX	AA067541;	
AC		
XX	05-AUG-1995	(first entry)
XX		
DE	Human flt-3 ligand.	
XX		
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..26
FT		/label= Sig_peptide
FT		/note= "signal peptide may extend to position 27"
FT		27..182
FT	Domain	/label= "extracellular domain
FT		/note= "extracellular domain may start at position 28"
FT		
FT	Domain	183..205
FT		/label= "transmembrane domain
FT		206..235
FT	Domain	/label= Cytoplasmic_domain
XX		
PN	EP627487-A.	
XX		
PD	07-DEC-1994.	
XX		
PF	19-MAY-1994;	94EP-0303575.
XX		
PR	24-MAY-1993;	93US-0068394.
PR	12-AUG-1993;	93US-0106463.
PR	25-AUG-1993;	93US-0111758.
PR	03-DEC-1993;	93US-0162407.
PR	07-MAR-1994;	94US-0209502.
PR	11-MAY-1994;	94US-0243545.
XX		
PA	(IMV) IMMUNEX CORP.	
XX		
PI	Beckmann MP, Lyman SD;	
XX		
DR	WPI; 1995-008071/02.	
DR	N-PSDB; AA079079.	
XX		
PT	Isolated ligands for flt 3 receptors - useful for treating	
XX	anaemia, AIDS and various cancers	
PS		
PS	Disclosure; Page 29-30; 33pp; English.	
XX		
CC	A human T-cell lambda-gli0 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AA079076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and stem cells, and can be used e.g. in gene therapy protocols.	
CC		
XX	Sequence	235 AA;

Query Match	63.2%	Score 772.5	DB 22	Length 235
Best Local Similarity	70.7%	Pred. No. 1.2e-65		
Matches 164	Conservative 17	Mismatches 42	Indels 9	Gaps 4
Qy	1	MTVAAPMSPNSLLLLLLLPCLNGPTGDCFFSHSPISNFKYKFRETNDHLKDPVT	60	
		: : : : : : : : : : : :		
Db	1	mtvlapwsp-tyll sglsqtdcsgfnpssldavxlreldsgyllqdyprv	59	
Qy	61	VAVNLODEKCKKALMSFLAQKRIEDLKVIVASSKQTLLEDVYNEIRHVSCTQPIPEC	120	
		: : : : : : :		
Db	60	vasnlqdeelcgalwtvlvraqrmerlcvassgkmqgllerynteihvfkcalqppsc	119	

Query Match	62.8%;	Score 768.5;	DB 16;	Length 235;
Best Local Similarity	70.3%;	Pred. No. 3e-69;		
Matches 163;	Conservative 17;	Mismatches 43;	Indels 9;	Gaps 4;

Query Match 62.8%; Score 768.5; DB 20; Length 235,

disorder (e.g. allergy, autoimmunity or immunosuppression). The protein

CC may be used to treat a pathological condition e.g. myelodysplasia,
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
CC leukemia.

XX Sequence 235 AA:

Query Match 62.8%; Score 768.5; DB 21; Length 235;
Best Local Similarity 70.3%; Pred. No. 3e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYVLAPAMSPNSLLILLLISPCLRGPPDCYFSPHSPISSNFKRFRLETHLKDVPVT 60
Db 1 mvlapawsp-ctylllllllllssglsqdcdfqhspsidfavkktrelsdyllqdyprt 59
QY 61 VAVNLQDEKHCALMSLFLAQRIEQLKTAVGSKMOTLLEDVNTIEHFVISCFOPLPEC 120
Db 60 vasnlqdeekcgllwrlvlaqrmwmerlktvagskngllervnteihfvkcafqppsc 119
QY 121 LRFVQTNISHLKDCOTQLAKPCIGKACONFSRCLEWOCOPSSSTLLPPRSPIALEAT 180
Db 120 lrfvqtnisrlllqetseqivaikpwlttr--qnfsrclelqcpdsscllppwsprrpleat 177
QY 181 ELPEPRPRLDLLLILFLPTVLVLAAGLWQARARR---GELHFGVPLP 228
Db 178 aptapqpp--llllllllpyglllllaawclhmqrtrrrtrppgqgvpvppsp 227

RESULT 17

AA020192 ID AAB20192 standard; Protein; 235 AA.

XX AAB20192;

XX 14-MAY-2001 (first entry)

XX Human Flt-3 ligand.

XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;

KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;

KW lymphoma; autoimmune disease; infection; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..26 /Label= Signal_peptide

FT Protein 27..235 /Label= Mature_protein

FT Domain 27..182 /Label= Extracellular_domain

FT Domain 183..205 /Label= Transmembrane_domain

FT Domain 206..235 /Label= Cytoplasmic_domain

XX WO200109303-A2.

PD 08-FEB-2001.

PF 31-JUL-2000; 2000WO-US20679.

XX 30-JUL-1999; 99US-0146170.

XX (VICA-) VICAL INC.

XX Hermanson GG;

XX WPI, 2001-123319/13.

DR N-PSDB; AAF30310.

XX Immunogenic compositions comprising Flt-3 ligand encoding

PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -

XX Claim 2; Page 132-133; 149pp; English.

CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
CC or 27-235 of the ligand. The polynucleotides are incorporated
CC into the cells of the vertebrate in vivo, and a prophylactically
CC or therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

XX Sequence 235 AA:

Query Match 62.8%; Score 768.5; DB 22; Length 235;
Best Local Similarity 70.3%; Pred. No. 3e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYVLAPAMSPNSLLILLLISPCLRGPPDCYFSPHSPISSNFKRFRLETHLKDVPVT 60
Db 1 mvlapawsp-ctylllllllllssglsqdcdfqhspsidfavkktrelsdyllqdyprt 59
QY 61 VAVNLQDEKHCALMSLFLAQRIEQLKTAVGSKMOTLLEDVNTIEHFVISCFOPLPEC 120
Db 60 vasnlqdeekcgllwrlvlaqrmwmerlktvagskngllervnteihfvkcafqppsc 119
QY 121 LRFVQTNISHLKDCOTQLAKPCIGKACONFSRCLEWOCOPSSSTLLPPRSPIALEAT 180
Db 120 lrfvqtnisrlllqetseqivaikpwlttr--qnfsrclelqcpdsscllppwsprrpleat 177
QY 181 ELPEPRPRLDLLLILFLPTVLVLAAGLWQARARR---GELHFGVPLP 228
Db 178 aptapqpp--llllllllpyglllllaawclhmqrtrrrtrppgqgvpvppsp 227

RESULT 18

AA058210 ID AAY58210 standard; Protein; 291 AA.

XX AAY58210;

XX 14-MAR-2000 (first entry)

XX Feline Flt-3 ligand.

XX Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Fells catus.

XX WO9961618-A2.

XX 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.
PR (HESK-) HESKA CORP.
PA
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
DR N-PSDB; AA255518, AA255519, AA255520, AA255521.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease -
XX
PS Claim 3c: Page 186-187; 264pp; English.
XX
XX Sequences AAY58204 and AAY58206-Y58209 respectively represent
CC encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
CC sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
CC ligand. The invention relates to canine Interleukin-4 (IL-4),
CC canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
CC Interferon-alpha (IFN-alpha), and nucleotides which encode these
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense
CC oligonucleotides). The proteins may be used to raise antibodies and to
CC screen for modulators of activity, while the antibodies may be used in
CC detection, and in drug targeting.
XX
SQ Sequence 291 AA:

Query Match 62.2%; Score 761; DB 21; Length 291;
Best Local Similarity 71.1%; Pred. No. 2,2e-68;
Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

QY 1 MYVLAAPMSNSSLLLLLSPLCRGTPDCYFSHSPISSNFKYKRELTDHLKDPVY 60
DB 1 mivlapawspfts-lllllllspglrpspcsfshspisctfkytlrklsydlldyptv 59

QY 61 VAVNLQDEKCKALMSLFLAQRMIQRLKTAVGSKMQTLLEDVNTEIHFTVTSCTFQPLPEC 120
DB 60 vaenlddelcpgfwhlvlaqgwmgrlkavagsgmqslleavnteihvltcatqdpisc 119

QY 121 LRVQYINISHLKDTCTQLALAKPCIGKACONFSRCLEVCQOPDSSTLLPPRSIALEAT 160
DB 120 lrvqytnisllldqtsqiaalkpwltf--nifsgclelqcpdssstlpprsialeat 177

QY 181 ELPEPREROLLLLPLTLVLAAMGLRWQARRR 218
DB 178 alpapq-apllllllllpvailllmsaawclhwrrrrr 214

RESULT 19
ID AAY69721 standard; Protein; 212 AA.
XX
AC AAY69721:
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein L-3H.
XX
KW 'Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;

KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200001823-A2.
XX
XX 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Graddis TJ, McGrew JT;
XX WPI: 2000-182115/16.
XX
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
XX immune response stimulation or treatment of pathological conditions
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
PS Claim 4; Page 79-80; 90pp; English.
XX
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
XX which exhibits increased or decreased biological activity relative to
XX the full length wild type (AAY69719) or mature (AAY69720) flt3-L
XX polypeptides. This sequence represents an example of the novel flt-3
XX ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
XX binds cell surface tyrosine kinase receptors and regulate growth and
XX differentiation of hematopoietic progenitor cells. The flt3-L protein can
XX be used to induce cellular expansion (especially in vivo) or
XX differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
XX cells, especially in the presence of growth factors such as interleukins,
XX colony stimulating factors or protein kinases. The protein can also
XX modulate, augment or enhance a patient's immune response and can be used
XX to treat an immune disorder (e.g. allergy, autoimmunity or
XX immunosuppression). The protein may be used to treat a pathological
XX condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
XX small cell lung, testicular or ovarian cancer, lymphoma, multiple
XX myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 212 AA:

Query Match 56.6%; Score 692; DB 21; Length 212;
Best Local Similarity 69.9%; Pred No. 1.3e-61;
Matches 144; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 27 GTPDCYFSHSPISSNFKYKRELTDHLKDPVYAVNLQDEKCKALMSLFLAQRMIQ 86
DB 3 gtgdcsfhspisdcfsvkirelsdyllldyptvasnlgdeecglwrlvlaqgmrer 62

QY 87 LKTAVGSKMQTLLEDVNTEIHFTVTSCTFQPLPECIRFQYNTNISHLKTCTQLALAKPCI 146
DB 63 lktvagskmgllervnteihvltckatqppscrlrtyqtnisllldqtsqiaalkpwlt 122

QY 147 GKACONFSRCLEVCQOPDSSTLLPPRSIALEATELPEPREROLLLLPLTLVLAAMGL 206
DB 123 tr--gnfscrlclqcpdssstlpprspplleatpqp--llllllllpvglllila 178

QY 207 AWGLRWQARRR-----GELHPGVLP 228
DB 179 awclhwgtrrrrrtrprrpgeqvpvrrp 204

RESULT 20
ID AAY69724

ID AAY69724 standard; protein; 209 AA.
 XX
 AC AAY69724;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Human flt-3 mutein K84T.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PE 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 4: Page 85-86; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the K84T mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX
 XX Sequence 209 AA:
 SQ
 Query Match 56.2%; Score 687; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 4, 2e-61;
 Matches 143; Conservative 16; Mismatches 38; Indels 8; Gaps 3;
 QY 28 TPDCTYSHSPISSEKFKREITDHLKDYPTVAVNLODEKHKALMSLELAQRWIEQL 87
 Db 1 tqdcsgfhpsidsdsvkirelsdyllqdyptvasnqdeqlcgylwrlvaqmerl 60
 QY 88 KTVAGSGMOTLEDVNTETHFVTSCTFOPLRCLRPVOTNISHLKDKCQDLALKPQIG 147
 Db 61 ktvagskmgjllervntehvltcafpptcrlfvqnsrllqgeseqivaqkpwit 120
 QY 148 KACQNSRCLLEVQCQPSSTLLPPRSPIALEATELPEPRPROLLLLLLPLTVLAAA 207

Db 121 r--gnfscrlclqcgqdsstlppwsprrleatpabpp--lllllllpvllllnaa 176
 QY 208 WGLRWQRRARR---GELHPGVPLP 228
 Db 177 wclhwgrtrrrtrprpgeqvpvppsp 201
 RESULT 21
 AAM69007
 ID AAM69007 standard; peptide; 209 AA.
 XX
 AC AAM69007;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Human flt-3 receptor agonist.
 XX
 KW Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
 KW bone marrow reconstitution; haematological disease; immune deficiency;
 KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
 KW congenital metabolic disease; neurological disease; therapy;
 KW dendritic cell production.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO9818923-A1.
 XX
 PD 07-MAY-1998.
 XX
 PE 23-OCT-1997; 97WO-US18700.
 XX
 PR 25-OCT-1996; 96US-0030094.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Feng Y, McKearn JP, McWhirter CA, Minnerly JC, Munster NJ;
 PI Staten NR, Streeter PR, Wolfe SL;
 DR WPI; 1998-272218/24.
 XX
 PT Rearranged flt-3 receptor agonists and nucleic acids encoding them -
 PT to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of haematological diseases, bone marrow reconstitution
 PT and in gene therapy
 XX
 PS Disclosure: Page 9-10; 158pp; English.
 XX
 CC This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or refold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.
 CC
 XX
 XX Sequence 209 AA:
 SQ
 Query Match 56.1%; Score 686; DB 19; Length 209;
 Best Local Similarity 69.8%; Pred. No. 5, 3e-61;

Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSNFKVRELTDLKDYPTAVANLQDEKCKALMSFLAQRWITQL 87
 Db 1 tqdcsfqhspsissdfavkirelsdyllqdyptvasnldqdeicggwrlvlaqrwmerl 60

QY 88 KTVAGSKMOTLLEDDVNTTEHFVTSCTFQPLPECLRFVQTNISHLKDKCTQTLALKPCIG 147
 Db 61 ktvagskmgqllervntelhfvtkcafgppscrlfvgtnisrlllgsetseqvalkpwit 120

QY 148 KACQNFSCLEVOCPDSSSTLLPPRSPIALATELPEPRPQQLLLLLPLTVLILAAA 207
 Db 121 r--qntsrcltqcpdssstlppwsprrleatlapqp--lllllllpvglllllaaa 176

QY 208 WGLRMQRRRR---GELHPGVLP 228
 Db 177 wclhwgrtrrrtrpprpegyvpvpsp 201

RESULT 22

AAV69720
 ID AAV69720 standard; Protein; 209 AA.

XX AC AAV69720;

XX DT 05-JUL-2000 (first entry)

XX DE Mature wild type human flt-3 protein.

XX KM Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia.

XX OS Homo sapiens.

XX PN WO200001823-A2.

XX PD 13-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14296.

XX PR 02-JUL-1998; 98US-0109100.

XX PA (IMMV) IMMUNEX CORP.

XX PI Graddis TJ, McGrew JT;

XX DR WPI: 2000-182115/16.

XX DR N-PSDB; AA259064.

XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -

XX PS Claim 1; Page 89-90; 90pp; English.

XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,

CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.

XX SQ Sequence 209 AA;

Query Match 56.1%; Score 686; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 5,3e-61;
 Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSNFKVRELTDLKDYPTAVANLQDEKCKALMSFLAQRWITQL 87
 Db 1 tqdcsfqhspsissdfavkirelsdyllqdyptvasnldqdeicggwrlvlaqrwmerl 60

QY 88 KTVAGSKMOTLLEDDVNTTEHFVTSCTFQPLPECLRFVQTNISHLKDKCTQTLALKPCIG 147
 Db 61 ktvagskmgqllervntelhfvtkcafgppscrlfvgtnisrlllgsetseqvalkpwit 120

QY 148 KACQNFSCLEVOCPDSSSTLLPPRSPIALATELPEPRPQQLLLLLPLTVLILAAA 207
 Db 121 r--qntsrcltqcpdssstlppwsprrleatlapqp--lllllllpvglllllaaa 176

QY 208 WGLRMQRRRR---GELHPGVLP 228
 Db 177 wclhwgrtrrrtrpprpegyvpvpsp 201

RESULT 23

AAV69723
 ID AAV69723 standard; Protein; 209 AA.

XX AC AAV69723;

XX DT 05-JUL-2000 (first entry)

XX DE Human flt-3 muteln K84E.

XX KM Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia; muteln.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200001823-A2.

XX PD 13-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14296.

XX PR 02-JUL-1998; 98US-0109100.

XX PA (IMMV) IMMUNEX CORP.

XX PI Graddis TJ, McGrew JT;

XX DR WPI: 2000-182115/16.

XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -

XX PS Claim 4; Page 84-85; 90pp; English.

XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3

CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX Sequence 209 AA;

Query Match 56.1%; Score 686; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 5.3e-61;

Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSENFVKRELTDHLKDYPTVAVNLODEKCKALMSFLAQWIEQL 87
 Db 1 tqdcstqshpsisdvfkirelsdyllqdyptvasnlgdeecgylwrlvlaqrmerl 60
 QY 88 KTVAGSKMOTLEDVNTTEHFVTSCTFQPLPECLRFVQTNISHLKDYCTOLAKPCIG 147
 Db 61 ktvagskmqglilervntelhfvtceafqppscrlfvqtnisrllqgeseqvalxprlt 120
 QY 148 KACQNSRCLEVOCCPDSTLLPSPRIALETELPEPRPQQLLLLLPLTVLAA 207
 Db 121 r--qnsrclqlqcpdsstlppwspripaleatlapqpp--lllllllpvgllllaaa 176
 QY 208 WGLRMQRRARR---GELHPGVPLP 228
 Db 177 wclhwqtrrrrrprpgeqyvpvpsp 201

RESULT 24

AAV69725
 ID AAV69725 standard; Protein; 209 AA.

XX AAV69725;

XX 05-JUL-2000 (first entry)

DE Human flt-3 mutein W118R.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.

OS Homo sapiens.
 OS Synthetic.

XX WO200001823-A2.

PD 13-JAN-2000.

XX 25-JUN-1999; 99WO-US14296.

XX 02-JUL-1998; 98US-0109100.

XX (IMMV) IMMUNEX CORP.

XX Gradis TJ, McGrew JT;

XX WPI; 2000-182115/16.
 XX

PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 PS Claim 4; Page 86-87; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibit increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the W118R mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX Sequence 209 AA;

Query Match 56.0%; Score 685; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 6.7e-61;

Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSENFVKRELTDHLKDYPTVAVNLODEKCKALMSFLAQWIEQL 87
 Db 1 tqdcstqshpsisdvfkirelsdyllqdyptvasnlgdeecgylwrlvlaqrmerl 60
 QY 88 KTVAGSKMOTLEDVNTTEHFVTSCTFQPLPECLRFVQTNISHLKDYCTOLAKPCIG 147
 Db 61 ktvagskmqglilervntelhfvtceafqppscrlfvqtnisrllqgeseqvalxprlt 120
 QY 148 KACQNSRCLEVOCCPDSTLLPSPRIALETELPEPRPQQLLLLLPLTVLAA 207
 Db 121 r--qnsrclqlqcpdsstlppwspripaleatlapqpp--lllllllpvgllllaaa 176
 QY 208 WGLRMQRRARR---GELHPGVPLP 228
 Db 177 wclhwqtrrrrrprpgeqyvpvpsp 201

RESULT 25

AAV69726
 ID AAV69726 standard; Protein; 209 AA.

XX AAV69726;

XX 05-JUL-2000 (first entry)

DE Human flt-3 mutein Q122R.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.

OS Homo sapiens.
 OS Synthetic.

XX WO200001823-A2.

XX 13-JAN-2000.
 XX

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:44:48 ; Search time 201.6 Seconds

(without alignments)
403.311 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MYTLAPAWSPNSLLILL.....WQARRRGELHPCVLPSPHP 231

Scoring table: BLOSUM62

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCPNUS.COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	1	PCT-US98-12085-2
2	1223	100.0	231	4	US-08-068-394-2
3	1223	100.0	231	5	US-08-106-463-2
4	1223	100.0	231	5	US-08-111-758-2
5	1223	100.0	231	5	US-08-162-407-2
6	1223	100.0	231	8	US-08-444-625-2
7	1223	100.0	231	8	US-08-444-626-2

8	1223	100.0	231	8	US-08-444-632-2	Sequence 2, Appl1
9	1223	100.0	231	10	US-08-669-697-2	Sequence 2, Appl1
10	1223	100.0	231	12	US-08-877-421-2	Sequence 2, Appl1
11	1223	100.0	231	18	US-09-448-378-2	Sequence 2, Appl1
12	1223	100.0	231	20	US-09-629-430B-8	Sequence 8, Appl1
13	1223	100.0	231	23	US-09-983-806-2	Sequence 2, Appl1
14	1223	100.0	231	24	US-10-095-449-2	Sequence 2, Appl1
15	1212.5	99.1	232	5	US-08-155-111-38	Sequence 38, Appl1
16	1212.5	99.1	232	5	US-08-162-413-38	Sequence 38, Appl1
17	1212.5	99.1	232	6	US-08-261-553-38	Sequence 38, Appl1
18	1212.5	99.1	232	6	US-08-472-168-38	Sequence 38, Appl1
19	1212.5	99.1	232	8	US-08-484-882-38	Sequence 38, Appl1
20	1212.5	99.1	232	8	US-08-486-661-38	Sequence 38, Appl1
21	1208.5	98.8	232	20	US-09-629-430B-13	Sequence 13, Appl1
22	1006	82.3	286	19	US-09-501-097-25	Sequence 25, Appl1
23	1006	82.3	287	19	US-09-501-097A-25	Sequence 25, Appl1
24	1004	82.1	189	20	US-09-629-430B-9	Sequence 9, Appl1
25	879	71.9	220	20	US-09-629-430B-17	Sequence 17, Appl1
26	879	71.9	220	20	US-09-629-430B-11	Sequence 11, Appl1
27	879	71.9	220	20	US-09-629-430B-15	Sequence 15, Appl1
28	774	63.3	294	17	US-09-322-409-7	Sequence 7, Appl1
29	774	63.3	294	18	US-09-451-527-7	Sequence 7, Appl1
30	772.5	63.2	235	5	US-08-155-111-34	Sequence 34, Appl1
31	772.5	63.2	235	5	US-08-162-413-34	Sequence 34, Appl1
32	772.5	63.2	235	6	US-08-261-553-34	Sequence 34, Appl1
33	772.5	63.2	235	8	US-08-472-168-34	Sequence 34, Appl1
34	772.5	63.2	235	8	US-08-484-882-34	Sequence 34, Appl1
35	772.5	63.2	235	8	US-08-486-661-34	Sequence 34, Appl1
36	772.5	63.2	235	20	US-09-629-430B-23	Sequence 23, Appl1
37	768.5	62.8	235	1	PCT-US98-12085-4	Sequence 4, Appl1
38	768.5	62.8	235	5	US-08-106-463-6	Sequence 6, Appl1
39	768.5	62.8	235	5	US-08-111-758-6	Sequence 6, Appl1
40	768.5	62.8	235	5	US-08-162-407-6	Sequence 6, Appl1
41	768.5	62.8	235	8	US-08-444-625-6	Sequence 6, Appl1
42	768.5	62.8	235	8	US-08-444-626-6	Sequence 6, Appl1
43	768.5	62.8	235	8	US-08-444-632-6	Sequence 6, Appl1
44	768.5	62.8	235	10	US-08-669-692-6	Sequence 6, Appl1
45	768.5	62.8	235	12	US-08-877-421-4	Sequence 4, Appl1
46	768.5	62.8	235	18	US-09-448-378-1	Sequence 1, Appl1
47	768.5	62.8	235	20	US-09-629-430B-19	Sequence 19, Appl1
48	768.5	62.8	235	22	US-09-891-498-1	Sequence 1, Appl1
49	768.5	62.8	235	23	US-09-904-536-1	Sequence 1, Appl1
50	768.5	62.8	235	23	US-09-983-806-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
Sequence 2, Application PC/TUS9812085
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, Version 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

```

1      REGISTRATION NUMBER: 32,655
2      REFERENCE/DOCKET NUMBER: 2855-WO
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (206) 587-0430
5      TELEFAX: (206) 233-0644
6      TELEX: 756622
7
8      INFORMATION FOR SEQ ID NO: 2 :
9      SEQUENCE CHARACTERISTICS:
10     LENGTH: 231 amino acids
11     TYPE: amino acid
12     TOPOLOGY: linear
13
14     MOLECULE TYPE: protein
15
16     CDT-US98-12085-2

```

Query Match	100.0%;	Score 1223;	DB 1;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 2.7e-110;		
Matches 231; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 1 MVLAPAWSPNSLLLLLLSPCLRGPDPDCFHSPISSNFKVKFRELTDHLIKDYPVT 60
 |||||
 1 MVLAPAWSPNSLLLLLLSPCLRGPDPDCFHSPISSNFKVKFRELTDHLIKDYPVT 60

	61	VANNLQDEKHKALMSLFIAQRWIEQLKTVAGSKMÖLLIEDVANTEIHFEVTSCTFQPLPEC	120
QY			
Dö	61	VAVNLQDEKHKALMSLFIAQRWIEQLKTVAGSKMÖLLIEDVANTEIHFEVTSCTFQPLPEC	120

Qy	121 LREVQTINISHLKDPCTCTQLLALPKPCIGKACQNFSRCLEVOCPDPSSTLLPPRSPIALEAT	180
D6	121 LREVQTINISHLKDPCTCTQLLALPKPCIGKACQNFSRCLEVOCPDPSSTLLPPRSPIALEAT	180

QY	Db
181	ELPEERPRQLLLLLLPLTVLLAAWGLRWQARRRGELHPGVPLPSHP 231
181	ELPEERPRQLLLLLLPLTVLLAAWGLRWQARRRGELHPGVPLPSHP 231

RESULT 2
US-08-068-394-2
: Sequence 2, Application US/08068394

1 GENERAL INFORMATION:
2 APPLICANT: Lyman, Stewart D.
3 APPLICANT: Beckmann, M. Patricia
4 TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
5
6 NUMBER OF SEQUENCES: 4
7
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
10 STREET: 51 University Street
11
12 CITY: Seattle
13
14 STATE: Washington
15
16 COUNTRY: US
17
18 ZIP: 98101

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

1 CLASSIFICATION: 435
2
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Malasaka, Stephen L.
5 REGISTRATION NUMBER: 32,655
6 REFERENCE/DOCKET NUMBER: 2813
7
8 TELECOMMUNICATION INFORMATION:
9
10 TELEPHONE: (206) 597-0430
11
12 TELEFAX: (206) 233-0644
13
14 TELETEX: 756822

```

; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 231 amino acids
;
; TYPE: AMINO ACID
;
; TOPOLOGY: linear
;

```

MOLECULE TYPE: protein
; US-08-068-394-2

Query Match	100.0%	Score 1223;	DB 4;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 2.7e-110;		
Matches 231; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MTVALAPAWSPNSLLLLLLLSPCLRGTDPDCYFHSPISSNFKVYKRELTDHLKDYPVT 60
Db 1 MTVALPAMWSNSSLLLLLLLSPCLRGTPDCCYFSHSPISSNFKVKFRELTDHLKDYPVT 60

Qy 61 VAVNIODEKCKALWLSFLAQRWIEQJKTAVAGSMOTLIEDVNEIHFWTSCTFQPLPEC 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 VAVNIODEKCKALWLSFLAQRWIEQJKTAVAGSMOTLIEDVNEIHFWTSCTFQPLPEC 120

```
OY      121 LRFVQTINISHLKDTQTLALPKPCIGKACQNFSRCLEFVCQDPDSSTLPPRSPALEAT 180
        |||||||
DB       121 LRFVQTINISHLKDTQTLALPKPCIGKACQNFSRCLEFVCQDPDSSTLPPRSPALEAT 180
```

QY 181 ELPEPRKQLLLLLLPLTLVLLAAWGLRWQRARRRGELHPGVLPSPH 231
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 ELPEPRKQLLLLLLPLTLVLLAAWGLRWQRARRRGELHPGVLPSPH 231

RESULT 3
US-08-106-463-2
Sequence 2, Application US/08106463

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for fli3/fliK-2 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

```

1 MEDIUM TYPE: Floppy disk
2
3 COMPUTER: IBM PC compatible
4
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6
7 SOFTWARE: Patent Release #1.0, Version #1.25
8
9 CURRENT APPLICATION DATA:
10
11 APPLICATION NUMBER: US/08/106,463
12
13 FILING DATE: 19930812
14
15 CLASSIFICATION: 435

```

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756622

```

; INFORMATION FOR SEQ ID NO: 2:
;
;   SEQUENCE CHARACTERISTICS:
;
;       LENGTH: 231 amino acids
;
;       TYPE: amino acid
;
;       TOPOLOGY: linear
;
;   MOLECULE TYPE: protein
;
US-08-106-463-2

```

Query Match	100.0%	Score 1223:	DB 5:	length 231;
Best Local Similarity	100.0%	Pred. No.	2.7e-110;	
Matches 231; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 MVLAPAMSPNSULLLLLLSPCLRGTPDCYFHSPISSNFKVKFRELTDHLKDPVT 60
|||||
1 MVLAPAMSPNSULLLLLLSPCLRGTPDCYFHSPISSNFKVKFRELTDHLKDPVT 60
Db

QY 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
DB 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 121 LRFVQTNISHLLKDKTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLLKDKTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLLLPLTLVLAANGLRMQRARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQLLLLLLLLPLTLVLAANGLRMQRARRRGELHPGVPLPSHP 231

RESULT 4
US-08-111-758-2
; Sequence 2, Application US/08111758
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION/DOCKET NUMBER: 32,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-758-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLAPAWSPNSLSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKLDYPT 60
DB 1 MYLAPAWSPNSLSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKLDYPT 60
QY 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
DB 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120

QY 121 LRFVQTNISHLLKDKTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLLKDKTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLLLPLTLVLAANGLRMQRARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQLLLLLLLLPLTLVLAANGLRMQRARRRGELHPGVPLPSHP 231

RESULT 5
US-08-162-407-2
; Sequence 2, Application US/08162407
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION/DOCKET NUMBER: 32,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-407-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLAPAWSPNSLSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKLDYPT 60
DB 1 MYLAPAWSPNSLSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKLDYPT 60
QY 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
DB 61 VAVNLODEKHCALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 121 LRFVQTNISHLLKDKTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180

Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVCQDPDSSTLLPPRSPITALEAT 180
QY 181 ELPEPRRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVPLDPSHP 231
Db 181 ELPEPRRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVPLDPSHP 231

RESULT 6

US-08-444-625-2
; Sequence 2, Application US/08444625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,625
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-625-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVYLAAPMWSNSSLILLLILSPCLRGTPDCYFSHSPISNFKYKRELTDHLKDYPT 60
Db 1 MTVYLAAPMWSNSSLILLLILSPCLRGTPDCYFSHSPISNFKYKRELTDHLKDYPT 60
QY 61 VAVNLODERCKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIELHFVTSCTFOPLPEC 120
Db 61 VAVNLODERCKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIELHFVTSCTFOPLPEC 120

QY 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVCQDPDSSTLLPPRSPITALEAT 180
Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVCQDPDSSTLLPPRSPITALEAT 180
QY 181 ELPEPRRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVPLDPSHP 231
Db 181 ELPEPRRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVPLDPSHP 231

RESULT 7

US-08-444-626-2
; Sequence 2, Application US/08444626
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-626-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVYLAAPMWSNSSLILLLILSPCLRGTPDCYFSHSPISNFKYKRELTDHLKDYPT 60
Db 1 MTVYLAAPMWSNSSLILLLILSPCLRGTPDCYFSHSPISNFKYKRELTDHLKDYPT 60
QY 61 VAVNLODERCKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIELHFVTSCTFOPLPEC 120
Db 61 VAVNLODERCKKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIELHFVTSCTFOPLPEC 120

Db 61 VAVNLDEKHCALMSLFLAQRMIEOLKTVAGSKMOTLLEVDNTEIHVTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQOPDSSTLLPRSPRIAEAT 180
Db 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQOPDSSTLLPRSPRIAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLWQRRARRRGEHLPGVPLPSHP 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLWQRRARRRGEHLPGVPLPSHP 231

RESULT 8
US-08-444-632-2
; Sequence 2, Application US/08444632

; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,632
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-632-2

Query Match 100.0%; Score 1223; DB 8; Length 231;

Best Local Similarity 100.0%; Pred. No. 2.7e-110; Mismatches 0; Indels 0; Gaps 0;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAAPWSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
Db 1 MTVLAAPWSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60

QY 61 VAVNLDEKHCALMSLFLAQRMIEOLKTVAGSKMOTLLEVDNTEIHVTSCTFOPLPEC 120
Db 61 VAVNLDEKHCALMSLFLAQRMIEOLKTVAGSKMOTLLEVDNTEIHVTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQOPDSSTLLPRSPRIAEAT 180
Db 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQOPDSSTLLPRSPRIAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAAGLWQRRARRRGEHLPGVPLPSHP 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAAGLWQRRARRRGEHLPGVPLPSHP 231

RESULT 9
US-08-669-692-2
; Sequence 2, Application US/08669692

; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-669-692-2

Query Match 100.0%; Score 1223; DB 10; Length 231;

Best Local Similarity 100.0%; Pred. No. 2.7e-110; Mismatches 0; Indels 0; Gaps 0;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAAPWSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
Db 1 MTVLAAPWSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60

Oy 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120
Db 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120
Oy 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Oy 181 ELPEPRRQOLLILLLLPLTLVLAAAGLWMQARRRGELHFGVPLPSHP 231
Db 181 ELPEPRRQOLLILLLLPLTLVLAAAGLWMQARRRGELHFGVPLPSHP 231

RESULT 10
US-08-877-421-2
Sequence 2, Application US/0887421
GENERAL INFORMATION:
APPLICANT: Viney, Joanne L.
APPLICANT: Mowatt, Allan MCI.
APPLICANT: Abbott, Nicholas
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune Tol
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,421
FILING DATE: 17-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-877-421-2

Query Match 100.0%; Score 1223; DB 12; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 ELPEPRRQOLLILLLLPLTLVLAAAGLWMQARRRGELHFGVPLPSHP 231

RESULT 11
US-09-448-378-2
Sequence 2, Application US/09448378
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 231
TYPE: PRT
ORGANISM: Mus sp.
US-09-448-378-2

Query Match 100.0%; Score 1223; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISNFKVKFRELDHLKNDYPVT 60
Db 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISNFKVKFRELDHLKNDYPVT 60
Oy 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120
Db 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120
Oy 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPIALEAT 180
Oy 181 ELPEPRRQOLLILLLLPLTLVLAAAGLWMQARRRGELHFGVPLPSHP 231
Db 181 ELPEPRRQOLLILLLLPLTLVLAAAGLWMQARRRGELHFGVPLPSHP 231

RESULT 12
US-09-629-430B-8
Sequence 8, Application US/09629430B
GENERAL INFORMATION:
APPLICANT: Hermanson, Gary George
TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
TITLE REFERENCE: 1530.0130001
CURRENT APPLICATION NUMBER: US/09/629,430B
CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/146,170
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 8
LENGTH: 231
TYPE: PRT
ORGANISM: Mus musculus
US-09-629-430B-8

Query Match 100.0%; Score 1223; DB 20; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISNFKVKFRELDHLKNDYPVT 60
Db 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISNFKVKFRELDHLKNDYPVT 60
Oy 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120
Db 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTLHFTVTSCTFOPLPEC 120

Db 61 VAAVNODEKHCALMSLFLAQRIWIEOLKTVAGSKMOTLEEDVNIHIVTSCTQPLPEC 120
QY 121 LRFVQTNISHLKDKTQTLALPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDKTQTLALPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRROLILLILLPLTVLVAAMGLRWQRARRRGEHLPGVPLPSHP 231
Db 181 ELPEPRROLILLILLPLTVLVAAMGLRWQRARRRGEHLPGVPLPSHP 231

RESULT 13
US-09-983-806-2
; Sequence 2, Application US/09983806
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,806
; FILING DATE: 25-Oct-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-983-806-2

Query Match 100.0%; Score 1223; DB 23; Length 231;
Best local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 VAAVNODEKHCALMSLFLAQRIWIEOLKTVAGSKMOTLEEDVNIHIVTSCTQPLPEC 120
Db 61 VAAVNODEKHCALMSLFLAQRIWIEOLKTVAGSKMOTLEEDVNIHIVTSCTQPLPEC 120
QY 121 LRFVQTNISHLKDKTQTLALPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDKTQTLALPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRROLILLILLPLTVLVAAMGLRWQRARRRGEHLPGVPLPSHP 231
Db 181 ELPEPRROLILLILLPLTVLVAAMGLRWQRARRRGEHLPGVPLPSHP 231

RESULT 14
US-10-095-449-2
; Sequence 2, Application US/10095449
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,449
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,692
; FILING DATE: 24-JUN-1996
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-095-449-2

Query Match 100.0%; Score 1223; DB 24; Length 231;
Best local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	61	VANNIODEHCKALMSLEIARWTEIOLKATVAGSKMOTLLEDVNETIHEVHSCTFOPIPEC	120
Db	61	VANNIODEHCKALMSLEIARWTEIOLKATVAGSKMOTLLEDVNETIHEVHSCTFOPIPEC	120
QY	121	LRPVONISHLIKDPCOTLAKRCKTRCAQONSRCLEVEQOCQPSSTLLPRSPALAEAT	180
Db	121	LRPVONISHLIKDPCOTLAKRCKTRCAQONSRCLEVEQOCQPSSTLLPRSPALAEAT	180
QY	181	ELDEPPRROLTLTLLEPLVTLVLLAAAMGRMQRARRRKEIHPGVLPDPSHP	241
Db	181	ELDEPPRROLTLTLLEPLVTLVLLAAAMGRMQRARRRKEIHPGVLPDPSHP	241

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	Similarity	99.1%	Score	1212.5	DB	5	Length	232
Best Local	Similarity	99.6%	Pred.	No. 2.8e-109				
Matches	231	Conservative	0	Mismatches	0	Indels	1	Gaps
QY	1	MTVLPAWSPNSLSLLLLLSLSPCLRGTPDDCYFSSHSPISNFKYKPRELIDHLKIDVPY	60					
Db	1	MTVLPAWSPNSLSLLLLLSLSPCLRGTPDDCYFSSHSPISNFKYKPRELIDHLKIDVPY	60					
QY	61	VAVNLDDEKHKALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTLHFWVSCFQPLPEEC	120					
Db	61	VAVNLDDEKHKALMSLFLAQRWIEQLKTVAGSKMQLLEEDVNTLHFWVSCFQPLPEEC	120					
QY	121	LRRVQNTNLSLLKIDTQTQLALPKPCIGACQNFSCLEVCQCPDPSSTLLPPRSFALERT	180					
Db	121	LRRVQNTNLSLLKIDTQTQLALPKPCIGACQNFSCLEVCQCPDPSSTLLPPRSFALERT	180					

QY 181 ELPERPRQ-LTLTLLPLTVLAAAGLRMRARRGELHPVLPSPH 231
||||| |||||||||
Db 181 ELPERPRQLLLLLLPLTVLAAAGLRMRARRGELHPVLPSPH 232

```

1 RESULT 16
2 US-08-162-413-38
3 Sequence 38. Application: US/08162413
4 GENERAL INFORMATION:
5 APPLICANT: Hannum, Charles H.
6 APPLICANT: Cuileper, Janice A.
7 APPLICANT: Lee, Frank D.
8 APPLICANT: Birnbaum, Daniel
9 TITLE OF INVENTION: Purified Mammalian Flt3 Ligands;
10 NUMBER OF SEQUENCES: 42
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: DNAX Research Institute
13 STREET: 901 California Avenue
14 CITY: Palo Alto
15 STATE: California
16 COUNTRY: USA
17 ZIP: 94304-1104
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: Patent In Release #1.0, Version #1.25
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/162,413
25 FILING DATE: 03-DEC-1993
26 CLASSIFICATION: 530
27 PRIORITY APPLICATION DATA:
28 APPLICATION NUMBER: US 08/155,111
29 FILING DATE: 19-NOV-1993
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/112,391
32 FILING DATE: 24-AUG-1993
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 08/106,340
35 FILING DATE: 13-AUG-1993
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 08/089,263
38 FILING DATE: 07-JUL-1993
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 08/065,231
41 FILING DATE: 19-MAY-1993
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Ching, Edwin P.
44 REGISTRATION NUMBER: 34,090
45 REFERENCE/DOCKET NUMBER: DX0350K5
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: 415-852-9196
48 TELEFAX: 415-496-1200
49 INFORMATION FOR SEQ ID NO: 38:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 232 amino acids
52 TYPE: amino acid
53 TOPOLOGY: linear
54 MOLECULE TYPE: protein
55 US-08-162-413-38

```

Query Match	99.1%	Score 1212.5	DB 5	Length 232
Best Local Similarity	99.6%	Pred. No. 2.8e-109		
Matches 231	Conservative 0	Mismatches 10	Indels 1	Gaps 1
QY	1	MTVLAPAMSPNSILLLLLLSPCLRGTPDCYFHSHPSSNFKKFKFRLDHLKDPY	60	
Db	1	MTVLAPAMSPNSILLLLLLSPCLRGTPDCYFHSHPSSNFKKFKFRLDHLKDPY	60	
QY	61	VAVNLDEKHCKALMSLFLAQRWIDQLTKVAGSKQILLDEVNTEIHFTVSCIPDLPKC	120	

Db 61 VAVNIODEKHCALMSLFLAQRWIEQLKTAVGSKMOTLLEVDNTEIHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLLKDTCTQLALKPCIGKACNFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLLKDTCTQLALKPCIGKACNFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRPRO-LILLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSHP 231
Db 181 ELPEPRROLILLILLPLTLVLLAAAGLRWQARRRGELHPGVLPSHP 232

RESULT 17
US-08-261-553-38

; Sequence 38, Application US/08261553

; GENERAL INFORMATION:

; APPLICANT: Hannum, Charles H.
; APPLICANT: Culpepper, Janice A.

; APPLICANT: Lee, Frank D.

; TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,553

; FILING DATE: 17-JUN-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,413

; FILING DATE: 03-DEC-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,111

; FILING DATE: 19-NOV-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,391

; FILING DATE: 24-AUG-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,340

; FILING DATE: 13-AUG-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,263

; FILING DATE: 07-JUL-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,231

; FILING DATE: 19-MAY-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0350K7

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196

; TELEFAX: 415-496-1200

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-553-38

Query Match

99.1%; Score 1212.5; DB 6; Length 232;

Best Local Similarity 99.6%; Pred. No. 2.8e-109; Indels 1; Gaps 1;
Matches 231; Conservative 0; Mismatches 0;

QY 1 MRYLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNFKYKFEELDHLKDYPTV 60

Db 1 MRYLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNFKYKFEELDHLKDYPTV 60

QY 61 VAVNIODEKHCALMSLFLAQRWIEQLKTAVGSKMOTLLEVDNTEIHFVTSCTFQPLPEC 120

Db 61 VAVNIODEKHCALMSLFLAQRWIEQLKTAVGSKMOTLLEVDNTEIHFVTSCTFQPLPEC 120

QY 121 LRFVQTNISHLLKDTCTQLALKPCIGKACNFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180

Db 121 LRFVQTNISHLLKDTCTQLALKPCIGKACNFSRCLEVOQCPDSSSTLLPPRSPIALEAT 180

QY 181 ELPEPRPRO-LILLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSHP 231

Db 181 ELPEPRROLILLILLPLTLVLLAAAGLRWQARRRGELHPGVLPSHP 232

RESULT 18
US-08-472-168-38

; Sequence 38, Application US/08472168

; GENERAL INFORMATION:

; APPLICANT: Hannum, Charles H.
; APPLICANT: Culpepper, Janice A.

; APPLICANT: Lee, Frank D.

; TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
; NUMBER OF SEQUENCES: 42; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,168

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,553

; FILING DATE: 17-JUN-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,413

; FILING DATE: 03-DEC-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,111

; FILING DATE: 19-NOV-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,391

; FILING DATE: 24-AUG-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,340

; FILING DATE: 13-AUG-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,263

; FILING DATE: 07-JUL-1993

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; REFERENCE/DOCKET NUMBER: DX0350K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-168-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2,8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDLKLDYPT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDLKLDYPT 60
QY 61 VAVNLQDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
DB 61 VAVNLQDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCQPSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCQPSSTLLPPRSPALAEAT 180
QY 181 ELPEPRPRO-LILLLLPLTVLLAAAGLWMQARRRGELHGVPLPSHP 231
DB 181 ELPEPRPRO-LILLLLPLTVLLAAAGLWMQARRRGELHGVPLPSHP 232

RESULT 19
US-08-484-882-38
; Sequence 38, Application US/08484882
; GENERAL INFORMATION:
; APPLICANT: Hannum, Charles H.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Lee, Frank D.
; APPLICANT: Birnbaum, Daniel
; TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: AGONISTS; ANTAGONISTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,882
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,553
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,413
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,111
; FILING DATE: 19-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,391
; FILING DATE: 24-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,340
; FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,263
; FILING DATE: 07-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,231
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0350K7GD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-882-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2,8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDLKLDYPT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDLKLDYPT 60
QY 61 VAVNLQDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
DB 61 VAVNLQDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCQPSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCQPSSTLLPPRSPALAEAT 180
QY 181 ELPEPRPRO-LILLLLPLTVLLAAAGLWMQARRRGELHGVPLPSHP 231
DB 181 ELPEPRPRO-LILLLLPLTVLLAAAGLWMQARRRGELHGVPLPSHP 232

RESULT 20
US-08-486-661-38
; Sequence 38, Application US/08486661
; GENERAL INFORMATION:
; APPLICANT: Hannum, Charles H.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Lee, Frank D.
; APPLICANT: Birnbaum, Daniel
; TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: AGONISTS; ANTAGONISTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,661
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0350K7GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-661-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2.8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
DB 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQ-LTLTLPLTVLLAAAGLWMORARRRGELHPVPLPSHP 231
DB 181 ELPEPRRQLTLTLPLTVLLAAAGLWMORARRRGELHPVPLPSHP 232

RESULT 21
US-09-629-430B-13
Sequence 13, Application US/09629430B
GENERAL INFORMATION:
APPLICANT: Hermanson, Gary George
TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
FILE REFERENCE: 1530.0130001
CURRENT APPLICATION NUMBER: US/09/629,430B
CURRENT FILING DATE: 2000-07-31
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 232
TYPE: PRP
ORGANISM: Mus musculus
US-09-629-430B-13

Query Match 98.8%; Score 1208.5; DB 20; Length 232;
Best Local Similarity 99.1%; Pred. No. 7e-109;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
DB 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQ-LTLTLPLTVLLAAAGLWMORARRRGELHPVPLPSHP 231
DB 181 ELPEPRRQLTLTLPLTVLLAAAGLWMORARRRGELHPVPLPSHP 232

DB 181 ELPEPRRQLTLTLPLTVLLAAAGLWMORARRRGELHPVPLPSHP 232

RESULT 22
US-09-501-097-25
Sequence 25, Application US/09501097
GENERAL INFORMATION:
APPLICANT: Tzyy-Chou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 02240-169349
CURRENT APPLICATION NUMBER: US/09/501,097
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 286
TYPE: PRP
ORGANISM: Human papillomavirus/Mouse
US-09-501-097-25

Query Match 82.3%; Score 1006; DB 19; Length 286;
Best Local Similarity 99.5%; Pred. No. 4.9e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
DB 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQL 190
DB 181 ELPEPRRQ 190

RESULT 23
US-09-501-097A-25
Sequence 25, Application US/09501097A
GENERAL INFORMATION:
APPLICANT: Tzyy-Chou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 287
TYPE: PRP
ORGANISM: Human papillomavirus/Mouse
US-09-501-097A-25

Query Match 82.3%; Score 1006; DB 19; Length 287;
Best Local Similarity 99.5%; Pred. No. 4.9e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
DB 1 MTYLAAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120

Tue Aug 6 09:34:38 2002

us-09-448-378-2.rpm

Page 13

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:41:14 ; Search time 38.79 Seconds
(without alignments)
899.284 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223
Sequence: 1 MVLAPAMSPNSLLILL.....WQARRRGELHPGVLPSPH 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 463719 seqs, 15109603 residues

Total number of hits satisfying chosen parameters: 463719

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/US06_NEM_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEM_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEM_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEM_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEM_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEM_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEM_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	US-60-368-263-2	Sequence 2, Appl1
2	768.5	62.8	235	PCR-US02-20172-4	Sequence 4, Appl1
3	768.5	62.8	235	US-60-368-263-1	Sequence 1, Appl1
4	763.5	62.4	235	PCR-US02-20172-5	Sequence 5, Appl1
5	568	46.4	156	US-10-053-355A-1	Sequence 1, Appl1
6	565.5	46.2	189	PCR-US02-20172-2	Sequence 2, Appl1
7	89.5	7.3	941	US-60-389-987-2466	Sequence 2466, Ap
8	88	7.2	1328	PCR-US02-18507-30	Sequence 30, Appl
9	88	7.2	1366	PCR-US02-18507-2	Sequence 2, Appl1
10	88	7.2	1366	PCR-US02-18507-6	Sequence 6, Appl1
11	88	7.2	1366	PCR-US02-18507-8	Sequence 8, Appl1
12	88	7.2	1366	PCR-US02-18507-10	Sequence 10, Appl
13	88	7.2	1366	PCR-US02-18507-12	Sequence 12, Appl
14	88	7.2	1366	PCR-US02-18507-14	Sequence 14, Appl
15	88	7.2	1366	PCR-US02-18507-16	Sequence 16, Appl
16	88	7.2	1366	PCR-US02-18507-18	Sequence 18, Appl
17	88	7.2	1366	PCR-US02-18507-20	Sequence 20, Appl
18	88	7.2	1366	PCR-US02-18507-22	Sequence 22, Appl
19	88	7.2	1366	PCR-US02-18507-24	Sequence 24, Appl
20	88	7.2	1366	PCR-US02-18507-26	Sequence 26, Appl
21	88	7.2	1366	PCR-US02-18507-28	Sequence 28, Appl
22	84.5	6.9	1205	PCR-US02-18211-1	Sequence 1, Appl1
23	84.5	6.9	1205	PCR-US02-18221-1	Sequence 1, Appl1
24	84.5	6.9	1205	US-10-164-890-1	Sequence 1, Appl1
25	83.5	6.8	425	US-10-168-365-35	Sequence 35, Appl
26	82.5	6.7	1266	US-09-011-307-12	Sequence 12, Appl

27	81.5	6.7	659	US-09-629-469A-14346	Sequence 14346, A
28	81.5	6.7	1148	US-60-389-987-1068	Sequence 1068, Ap
29	81	6.6	1965	PCR-US02-18507-4	Sequence 4, Appl1
30	81	6.6	4131	US-60-360-039-5136	Sequence 5136, Ap
31	80	6.5	245	US-09-629-469A-18532	Sequence 18532, A
32	80	6.5	811	US-09-991-150-57	Sequence 57, Appl
33	80	6.5	811	US-09-950-041-39	Sequence 39, Appl
34	80	6.5	811	US-10-121-062-414	Sequence 414, App
35	80	6.5	811	US-10-095-627-13	Sequence 13, Appl
36	80	6.5	811	US-10-173-699-414	Sequence 414, App
37	80	6.5	811	US-10-173-699-414	Sequence 414, App
38	80	6.5	811	US-10-173-691-414	Sequence 414, App
39	80	6.5	811	US-10-173-692-414	Sequence 414, App
40	80	6.5	811	US-10-173-692-414	Sequence 414, App
41	80	6.5	811	US-10-173-697-414	Sequence 414, App
42	80	6.5	811	US-10-173-698-414	Sequence 414, App
43	80	6.5	811	US-10-173-699-414	Sequence 414, App
44	80	6.5	811	US-10-173-701-414	Sequence 414, App
45	80	6.5	811	US-10-173-704-414	Sequence 414, App
46	80	6.5	811	US-10-173-708-414	Sequence 414, App
47	80	6.5	811	US-10-174-571-414	Sequence 414, App
48	80	6.5	811	US-10-174-574-414	Sequence 414, App
49	80	6.5	811	US-10-174-583-414	Sequence 414, App
50	80	6.5	811	US-10-173-694-414	Sequence 414, App

ALIGNMENTS

RESULT 1
US-60-368-263-2
; Sequence 2, Application US/60368263
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368, 263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp
US-60-368-263-2

Query Match 100.0%; Score 1223; DB 7; Length 231;
Best local Similarity 100.0%; Pred. No. 2e-105;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLAPAMSPNSLLILLSPCLRGTPDCYFSPTSSNFKYKFRRLDHLKDYPT 60
|||||
DB 1 MVLAPAMSPNSLLILLSPCLRGTPDCYFSPTSSNFKYKFRRLDHLKDYPT 60
QY 61 VAVNIDEXHCKALMSFLAORNIOLKTIVAGSKQOTLLEVNTEIHFVTSCTFOPPEC 120
|||||
DB 61 VAVNIDEXHCKALMSFLAORNIOLKTIVAGSKQOTLLEVNTEIHFVTSCTFOPPEC 120
QY 121 LRFVQNIHSLKDTCTQIALKPCIGRACQNFSCLEVOQOPDSSTLLPRSPALEAT 180
|||||
DB 121 LRFVQNIHSLKDTCTQIALKPCIGRACQNFSCLEVOQOPDSSTLLPRSPALEAT 180
QY 181 ELPEPPRQULLLLLLPLTLVILAAWGLRQARRRGELHPGVLPSPH 231
|||||
DB 181 ELPEPPRQULLLLLLPLTLVILAAWGLRQARRRGELHPGVLPSPH 231
RESULT 2
PCR-US02-20172-4
; Sequence 4, Application PC/TUS0220172

```

; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-4
```

```

Query Match          62.8%; Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%; Pred. No. 2.5e-63;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

```

QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSHSPISSNFKYKRELTDLHKDYPVT 60
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MTVALPAMSP--TYYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 VAVNLQDEKCKALMSLFLAQRWTEOLKTVAGSKMOTLEDVNTETHEFVTSCTFQPLPEC 120
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 VASNLQDEELCGGLMRVLAQRWMERLKTIVAGSKMOTLEDVNTETHEFVTKCAFQPPSC 119
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCPDSSTLLPPSPALAEAT 180
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 LRFVQTNISRLQETSQTLVALKPWITR--QNFSCRLELCQCPDSSTLLPPSPALAEAT 177
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVLP 228
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLRMQRRAR---GELHPGVLP 227
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```

RESULT 3
US-60-368-263-1
; Sequence 1, Application US/60368263
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLU-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-368-263-1
```

```

Query Match          62.8%; Score 768.5; DB 7; Length 235;
Best Local Similarity 70.3%; Pred. No. 2.5e-63;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

```

QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSHSPISSNFKYKRELTDLHKDYPVT 60
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MTVALPAMSP--TYYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 VAVNLQDEKCKALMSLFLAQRWTEOLKTVAGSKMOTLEDVNTETHEFVTSCTFQPLPEC 120
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 VASNLQDEELCGGLMRVLAQRWMERLKTIVAGSKMOTLEDVNTETHEFVTKCAFQPPSC 119
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCPDSSTLLPPSPALAEAT 180
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 LRFVQTNISRLQETSQTLVALKPWITR--QNFSCRLELCQCPDSSTLLPPSPALAEAT 177
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```

QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVLP 228
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLRMQRRAR---GELHPGVLP 227
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```

RESULT 4
PCT-US02-20172-5
; Sequence 5, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-5
```

```

Query Match          62.4%; Score 763.5; DB 1; Length 235;
Best Local Similarity 69.8%; Pred. No. 7.2e-63;
Matches 162; Conservative 17; Mismatches 44; Indels 9; Gaps 4;
```

```

QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSHSPISSNFKYKRELTDLHKDYPVT 60
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MTVALPAMSP--TYYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 VAVNLQDEKCKALMSLFLAQRWTEOLKTVAGSKMOTLEDVNTETHEFVTSCTFQPLPEC 120
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 VASNLQDEELCGGLMRVLAQRWMERLKTIVAGSKMOTLEDVNTETHEFVTKCAFQPPSC 119
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCPDSSTLLPPSPALAEAT 180
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 LRFVQTNISRLQETSQTLVALKPWITR--QNFSCRLELCQCPDSSTLLPPSPALAEAT 177
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVLP 228
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLRMQRRAR---GELHPGVLP 227
    |||||:::|||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```

RESULT 5
US-10-053-355A-1
; Sequence 1, Application US/10053355A
; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High
; FILE REFERENCE: A-70682/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/053,355A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/316,723
; PRIOR FILING DATE: 2001-08-31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-355A-1
```

```

Query Match          46.4%; Score 568; DB 6; Length 156;
Best Local Similarity 73.9%; Pred. No. 5.5e-45;
Matches 113; Conservative 12; Mismatches 26; Indels 2; Gaps 1;
```

```

QY 28 TPDCYFSHSPISSNFKYKRELTDLHKDYPVTAVAVNLQDEKCKALMSLFLAQRWTEOL 87
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-2466

Query Match
Best Local Similarity 46.2%; Score 565.5; DB 1; Length 189;
Matches 129; Conservative 12; Mismatches 36; Indels 55; Gaps 4;

QY 1 MTVALPAMSPSSLLILLISCLRGPDYCFHSPISSNFKVFRRLTDHLKDYPT 60
DB 1 MTVALPAMSP--TLYLLILLSSLSGLSTGDCSFQHSPISSDPAVKIRLSYLLQDYPVT 59
QY 61 VAVNLODEKCKALMSFLAQRNIEQLKTVAGSKMOTLLEDVNTIHFVTSCTQPLPEC 120
DB 60 VASINLODEELCGGLMRLVLAQRNMRERLKTVAAGSKMGLERVNTIHFVTCARQ----- 114
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCPDSTLLPPRSPLEAT 180
DB 115 -----DSTLLPPMSPRPLEAT 131
QY 181 ELPPRRQLLLILLPLVLVLAANGLRQGRARR-----GELHPGVPLP 228
DB 132 APTAPQPP--TLTLLPLVGLLLLAAMCLHMQRTRRTPRPGEQVPPVPS 181

RESULT 7
; Sequence 2466, Application US/60389987
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660098.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2466
; LENGTH: 941

PCT-US02-20172-2
; Sequence 2, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USFS THEREOF
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-2
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-2466

Query Match
Best Local Similarity 7.3%; Score 89.5; DB 7; Length 941;
Matches 24; Conservative 0; Mismatches 16; Indels 9; Gaps 2;

QY 183 PEPPRRQLLLILLPLVLVLAANGLRQGRARRGELHPGVPLPSHP 231
DB 15 PPPPPARLLILLPLLLPLIAPGANG--WANGARR-----PPPS 54

RESULT 8
PCT-US02-18507-30
; Sequence 30, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004M0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1928
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-30

Query Match
Best Local Similarity 7.2%; Score 88; DB 1; Length 1928;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPCCYSHSPISNNEKVKRELTDLK---DYVTVANNLODEKCKALM-----STFL 79
DB 1399 GVPD-----NLSFYK-----NHIMKRYDRPHKGT-KDENEFKSLMERTSYL 1445
QY 80 AQ-----RW--IEQLKTVAGSKMOT--LLEDVNTIHFVTSCTQPLPEC 121
DB 1446 VQSLPGISRMFEVEKREVMSPLENALIEVLNKNQOLKTLISOCOTROMONINPLTMCL 1505
QY 122 -----RFV 124
DB 1506 NGVIDAANGVSRGYQAFVYKCYILSHPEDEKTIARLRLMLDQAQTLERGLAVHKEFY 1565
QY 125 QTNISHLKDTCTQLALKPCIGKACONFSRCLEVO-----CQ-----PDS 165
DB 1566 PQDMRPPLHKLVDPFFVMKSSLG--IOEFSACMOQASPVHFPNGSPRYCRNSAPASVPDG 1623
QY 166 STLLPPRSPLEA 179
DB 1624 TRVTPRRSPLEA 1637

RESULT 9
PCT-US02-18507-2
; Sequence 2, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004M0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
```

```
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-2
```

```
Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
```

```
QY 27 GTPDCYFSHSPISSNFKVRFRELTDLK---DYPVYVAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSEYKV-----NHMKFRYDRPFHKGTK-DKENEFKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYISC-----TFQPLPECL 121
Db 1446 VQSLPGISRMFEVEKREYVEMSPLENALEVLNKNQOLKTLISOCQTRQMNINPLTMCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRQOAEFYKEYILSHPEDEGKIARLRLMLBOAQLFEGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCLEVO-----CQ-----PDS 165
Db 1566 PQDMRLHKKLVDOFYVMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
QY 166 STILLPRSPALAE 179
Db 1624 TRVIPRSPSLYPA 1637

RESULT 10
PCT-US02-18507-6
; Sequence 6, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-6
```

```
Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
```

```
QY 27 GTPDCYFSHSPISSNFKVRFRELTDLK---DYPVYVAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSEYKV-----NHMKFRYDRPFHKGTK-DKENEFKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYISC-----TFQPLPECL 121
Db 1446 VQSLPGISRMFEVEKREYVEMSPLENALEVLNKNQOLKTLISOCQTRQMNINPLTMCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRQOAEFYKEYILSHPEDEGKIARLRLMLBOAQLFEGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCLEVO-----CQ-----PDS 165
Db 1566 PQDMRLHKKLVDOFYVMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
QY 166 STILLPRSPALAE 179
Db 1624 TRVIPRSPSLYPA 1637
```

```
Db 1624 TRVIPRSPSLYPA 1637
```

```
RESULT 11
PCT-US02-18507-8
; Sequence 8, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-8
```

```
Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
```

```
QY 27 GTPDCYFSHSPISSNFKVRFRELTDLK---DYPVYVAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSEYKV-----NHMKFRYDRPFHKGTK-DKENEFKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYISC-----TFQPLPECL 121
Db 1446 VQSLPGISRMFEVEKREYVEMSPLENALEVLNKNQOLKTLISOCQTRQMNINPLTMCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRQOAEFYKEYILSHPEDEGKIARLRLMLBOAQLFEGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCLEVO-----CQ-----PDS 165
Db 1566 PQDMRLHKKLVDOFYVMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
QY 166 STILLPRSPALAE 179
Db 1624 TRVIPRSPSLYPA 1637
```

```
RESULT 12
PCT-US02-18507-10
; Sequence 10, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-10
```

```
Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
```

```
QY 27 GTPDCYFSHSPISSNFKVRFRELTDLK---DYPVYVAVNLQDEKCKALM-----SLFL 79
```

```
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISQCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIILSHPEDGEKIALRLMLBOAQILLEGFLAVHEKVF 1565
QY 125 QTNISHLKDTCTQLALPKCIGKACQNFSCLEVO-----CO-----PDS 165
Db 1566 PQDMRPLHKKLVDQFFVMKSLG--IQEFSACMQASPVHFPNGSPRVCRNSAPASVSPDG 1623
QY 166 STLPPRSPIALRA 179
Db 1624 TRVAPRSPLSTPA 1637

RESULT 13
PCT-US02-18507-12
; Sequence 12, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-12

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISNFKVRELTDHLK---DYPTAVANLQDEKHKALW---SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISQCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIILSHPEDGEKIALRLMLBOAQILLEGFLAVHEKVF 1565
QY 125 QTNISHLKDTCTQLALPKCIGKACQNFSCLEVO-----CO-----PDS 165
Db 1566 PQDMRPLHKKLVDQFFVMKSLG--IQEFSACMQASPVHFPNGSPRVCRNSAPASVSPDG 1623
QY 166 STLPPRSPIALRA 179
Db 1624 TRVAPRSPLSTPA 1637

RESULT 14
PCT-US02-18507-14
; Sequence 14, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
```

```
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-14

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISNFKVRELTDHLK---DYPTAVANLQDEKHKALW---SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISQCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIILSHPEDGEKIALRLMLBOAQILLEGFLAVHEKVF 1565

RESULT 15
PCT-US02-18507-16
; Sequence 16, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-16

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISNFKVRELTDHLK---DYPTAVANLQDEKHKALW---SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--IEOLKTVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISQCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIILSHPEDGEKIALRLMLBOAQILLEGFLAVHEKVF 1565
```



```
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1205
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18221-1
```

Query Match

6.9%; Score 84.5; DB 1; Length 1205;
Best Local Similarity 21.9%; Pred. No. 41;
Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

```
QY 40 SNFKVRELTDLKDYPTAVANLQDEKHKALMSFLAQRWIEQLTVAGSK----- 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 876 SDNKMVRSCEANKKRPFRMCNIOECTH-----PLWVAEWEHCHTKCGSSGYQLRT 930
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 ---MOTLEDVNTEIHV-----TSCFQPLP-----ECLRFV--QTNISH 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 931 VRCLQPLDGTNSVSHSKYCMGDRPSRRPCNRVPCPAQMTGPMSECSVTGEGTEVRQ 990
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 LL-----KDTCTQLLALKPCIGKAC-----QNSRCLEVOQC 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 991 VILCRAGDHCDGKEKPEVSRAQCLPNCNDPCLDGKSIFCOMEVLYARYCSIPGYNKLCCESC 1050
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 QPDSSTLLPRSPALAEATEL-----PEPRROLILLILLLP 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1051 SKRST-LPP--PYLLEAETHDDVYSNPSDLPRLSLVMTSLVP 1091
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 23

```
PCT-US02-18221-1
; Sequence 1, Application PC/TUS0218221
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel S.
; APPLICANT: Hirohata, Satoshi
; APPLICANT: Eyre, David
; APPLICANT: Fernandes, Russell
; TITLE OF INVENTION: ADAMTS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: 26336-10-1
; CURRENT APPLICATION NUMBER: PCT/US02/18221
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/296,384
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1205
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18221-1
```

Query Match 6.9%; Score 84.5; DB 1; Length 1205;
Best Local Similarity 21.9%; Pred. No. 41;
Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

```
QY 40 SNFKVRELTDLKDYPTAVANLQDEKHKALMSFLAQRWIEQLTVAGSK----- 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 876 SDNKMVRSCEANKKRPFRMCNIOECTH-----PLWVAEWEHCHTKCGSSGYQLRT 930
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 ---MOTLEDVNTEIHV-----TSCFQPLP-----ECLRFV--QTNISH 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 931 VRCLQPLDGTNSVSHSKYCMGDRPSRRPCNRVPCPAQMTGPMSECSVTGEGTEVRQ 990
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 LL-----KDTCTQLLALKPCIGKAC-----QNSRCLEVOQC 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 991 VILCRAGDHCDGKEKPEVSRAQCLPNCNDPCLDGKSIFCOMEVLYARYCSIPGYNKLCCESC 1050
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 QPDSSTLLPRSPALAEATEL-----PEPRROLILLILLLP 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1051 SKRST-LPP--PYLLEAETHDDVYSNPSDLPRLSLVMTSLVP 1091
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 24

```
US-10-164-890-1
; Sequence 1, Application US/10164890
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel S.
; APPLICANT: Hirohata, Satoshi
; APPLICANT: Eyre, David
; APPLICANT: Fernandes, Russell
; TITLE OF INVENTION: ADAMTS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: 26336-10-1
; CURRENT APPLICATION NUMBER: US/10/164,890
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/296,384
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-890-1
```

Query Match 6.9%; Score 84.5; DB 6; Length 1205;
Best Local Similarity 21.9%; Pred. No. 41;
Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

```
QY 40 SNFKVRELTDLKDYPTAVANLQDEKHKALMSFLAQRWIEQLTVAGSK----- 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 876 SDNKMVRSCEANKKRPFRMCNIOECTH-----PLWVAEWEHCHTKCGSSGYQLRT 930
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 ---MOTLEDVNTEIHV-----TSCFQPLP-----ECLRFV--QTNISH 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 931 VRCLQPLDGTNSVSHSKYCMGDRPSRRPCNRVPCPAQMTGPMSECSVTGEGTEVRQ 990
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 LL-----KDTCTQLLALKPCIGKAC-----QNSRCLEVOQC 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 991 VILCRAGDHCDGKEKPEVSRAQCLPNCNDPCLDGKSIFCOMEVLYARYCSIPGYNKLCCESC 1050
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 QPDSSTLLPRSPALAEATEL-----PEPRROLILLILLLP 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1051 SKRST-LPP--PYLLEAETHDDVYSNPSDLPRLSLVMTSLVP 1091
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 25

```
US-10-168-365-35
; Sequence 35, Application US/10168365
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Junli
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 30266/37650
; CURRENT APPLICATION NUMBER: US/10/168,365
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-365-35
```

Query Match 6.8%; Score 83.5; DB 6; Length 425;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd..

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:37 ; Search time 22.73 Seconds

(without alignments)
248.232 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MTVLAPAMSPNSLLILL.....MQRARRRGELHPGVLPSPHP 231

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1223	100.0	231	1	US-08-243-545-2
2	1223	100.0	231	2	US-08-993-962-2
3	1223	100.0	231	4	US-09-160-841-2
4	1223	100.0	231	5	PCT-US94-05365-2
5	1220	99.8	231	1	US-08-220-379B-7
6	1220	99.8	231	5	PCT-US95-03866-6
7	768.5	62.8	235	1	US-08-243-545-6
8	768.5	62.8	235	2	US-08-993-962-6
9	768.5	62.8	235	4	US-09-160-841-6
10	768.5	62.8	235	4	US-09-109-100-1
11	768.5	62.8	235	5	PCT-US94-05365-6
12	724.5	59.2	137	4	US-09-109-100-19
13	692	56.6	112	4	US-09-109-100-10
14	687	56.2	209	4	US-09-109-100-15
15	686	56.1	209	4	US-09-109-100-14
16	685	56.1	209	4	US-09-109-100-18
17	685	56.0	209	4	US-09-109-100-16
18	682	55.8	209	4	US-09-109-100-9
19	682	55.8	209	4	US-09-109-100-12
20	680	55.6	209	4	US-09-109-100-17
21	679	55.5	209	4	US-09-109-100-11
22	678	55.4	209	4	US-09-109-100-13
23	678	55.4	209	4	US-09-109-100-8
24	216	17.7	42	5	PCT-US94-05150-17
25	135	11.0	28	5	PCT-US84-05150-12
26	105	8.6	22	5	PCT-US94-05150-10
27	95.5	7.8	909	2	US-08-310-912A-142

28	95.5	7.8	909	4	US-09-301-085-142	Sequence 142, App
29	95.5	7.8	909	5	PCT-US95-04589-142	Sequence 142, App
30	92	7.5	885	2	US-08-310-912A-2	Sequence 2, Appl1
31	92	7.5	885	3	US-08-841-089-2	Sequence 2, Appl1
32	92	7.5	885	4	US-09-301-085-2	Sequence 2, Appl1
33	92	7.5	885	5	PCT-US95-04570-2	Sequence 2, Appl1
34	92	7.5	885	5	PCT-US95-04589-2	Sequence 2, Appl1
35	83.5	6.8	552	1	US-07-999-2800A-22	Sequence 2, Appl1
36	83.5	6.8	552	1	US-07-999-2800A-24	Sequence 24, Appl1
37	83.5	6.8	552	1	US-08-426-279-22	Sequence 24, Appl1
38	83.5	6.8	552	1	US-08-426-279-24	Sequence 24, Appl1
39	83.5	6.8	552	1	US-08-401-013-22	Sequence 22, Appl1
40	83.5	6.8	552	1	US-08-401-013-24	Sequence 22, Appl1
41	83.5	6.8	552	3	US-08-426-570-22	Sequence 22, Appl1
42	83.5	6.8	552	3	US-08-426-570-24	Sequence 22, Appl1
43	83.5	6.8	552	3	US-08-426-876-22	Sequence 22, Appl1
44	83.5	6.8	552	3	US-08-426-876-24	Sequence 24, Appl1
45	83.5	6.8	552	4	US-08-426-243-22	Sequence 24, Appl1
46	83.5	6.8	552	4	US-08-426-243-24	Sequence 24, Appl1
47	83.5	6.8	552	4	US-08-401-632-22	Sequence 24, Appl1
48	83.5	6.8	552	4	US-08-401-632-24	Sequence 24, Appl1
49	83.5	6.8	859	3	US-09-183-253-2	Sequence 2, Appl1
50	83.5	6.8	2476	2	US-08-276-967-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-243-545-2
; Sequence 2, Application US/08243545
; Patent No. 5534512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for fli3/fliK-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-2

Query Match 100.0%; Score 1223; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 6,9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLLLSPLCLRGTPDCYFSHSPISNFKVFRRLTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLLLSPLCLRGTPDCYFSHSPISNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDCTQLALAKPCIGKACONFSRCLEVOQCPDSTLLPRSPALAEAT 180
DB 121 LRFVQTNISHLKDCTQLALAKPCIGKACONFSRCLEVOQCPDSTLLPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPGVLPSPHP 231
DB 181 ELPEPRRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPGVLPSPHP 231

RESULT 2
US-08-993-962-2
Sequence 2, Application US/08993962
Patent No. 5843423
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2613-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-2

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 6,9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLLLSPLCLRGTPDCYFSHSPISNFKVFRRLTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLLLSPLCLRGTPDCYFSHSPISNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLDEKCKALMSFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDCTQLALAKPCIGKACONFSRCLEVOQCPDSTLLPRSPALAEAT 180
DB 121 LRFVQTNISHLKDCTQLALAKPCIGKACONFSRCLEVOQCPDSTLLPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPGVLPSPHP 231
DB 181 ELPEPRRQLLLLLPLTLVLVLAAMGLRWQARRRGELHPGVLPSPHP 231

RESULT 3
US-09-160-841-2
Sequence 2, Application US/09160841
Patent No. 6190655
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

1
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-2

Query Match 100.0%; Score 1223; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFSHSPISNNKVKFRELTHLKDYPVT 60
DB 1 MTVALPAMSPNSLSLILLLLSCLLGCTGDCIFSHSPISNNKVKFRELTHLKDYPVT 60
QY 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
DB 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
QY 181 ELPEPRROLILLLPLTVLVAAGLWQARRRGGELHPGVPLPSHP 231
DB 181 ELPEPRROLILLLPLTVLVAAGLWQARRRGGELHPGVPLPSHP 231

RESULT 4
PCT-US94-05365-2
Sequence 2, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFSHSPISNNKVKFRELTHLKDYPVT 60
DB 1 MTVALPAMSPNSLSLILLLLSCLLGCTGDCIFSHSPISNNKVKFRELTHLKDYPVT 60
QY 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
DB 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAAGSKMOTLLEDVNTETHEVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
QY 181 ELPEPRROLILLLPLTVLVAAGLWQARRRGGELHPGVPLPSHP 231
DB 181 ELPEPRROLILLLPLTVLVAAGLWQARRRGGELHPGVPLPSHP 231

RESULT 5
US-08-220-379B-7
Sequence 7, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: NO. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B

FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
PUBLICATION INFORMATION:
AUTHORS: Lyman, et al.
JOURNAL: Cell
PAGES: 1157-1167
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 231
US-08-220-3798-7

Query Match 99.8%; Score 1220; DB 1; Length 231;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 230; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
DB 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
QY 61 VAVNLDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
DB 61 VAVNLDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
QY 121 LRFQVNTISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
DB 121 LRFQVNTISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
QY 181 ELPEPRRQILLILLPLTLVLLAAAGLRMQRRARRGELHPGVLPDPSHP 231
DB 181 ELPEPRRQILLILLPLTLVLLAAAGLRMQRRARRGELHPGVLPDPSHP 231

RESULT 6
PCT-US95-03866-6
Sequence 6, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..205
PCT-US95-03866-6

Query Match 99.8%; Score 1220; DB 5; Length 231;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 230; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
DB 1 MTVALPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
QY 61 VAVNLDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
DB 61 VAVNLDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
QY 121 LRFQVNTISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
DB 121 LRFQVNTISHLKDTCTQLALKPCIGKACQNFSCLEVOQCPDSSSTLLPRSPALAEAT 180
QY 181 ELPEPRRQILLILLPLTLVLLAAAGLRMQRRARRGELHPGVLPDPSHP 231
DB 181 ELPEPRRQILLILLPLTLVLLAAAGLRMQRRARRGELHPGVLPDPSHP 231

RESULT 7
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:


```
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-243-545-6
```

```
Query Match 62.8%; Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

```
QY 1 MTVLAPAMSPSSLLILLSPCLNCTPDCTFSPHSPISSNKKVFRRLTHLLKDPVPT 60
DB 1 MTVLAPAMSP--TYYLILLLLSSLSGTSQDPSFQHSPISSDPAVKIRLSYLLQDYPVT 59
QY 61 VAVNLODEKHKALMSLFLAQRWTEQLKTIVAGSKMOTLLEDVNTLHFTVCTFQPLPEC 120
DB 60 VASNLQDELCGLMRLVLAQRWMERLKTIVAGSKMGLLERVNTEHFTVTCARQPPESC 119
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVCOPDSSSTLLPPRSPALAEAT 180
DB 120 LRFVQTNISRLQFTSQDLVALKFWITR--QNFSCRLELCQCPDSSSTLLPPWSPRPLEAT 177
QY 181 ELPEPRRQQLLLLLPLTVLLAAAGLWQARARR---GELHPGVLP 228
DB 178 APTAQP--LILLLLPVGLLLAAAGLHWQRTRRTPRGEQVPPVPS 227
```

```
RESULT 8
US-08-993-962-6
; Sequence 6, Application US/08993962
; Patent No. 5843423
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/993,962
; FILING DATE: December 18, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-993-962-6
```

```
Query Match 62.8%; Score 768.5; DB 2; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

```
QY 1 MTVLAPAMSPSSLLILLSPCLNCTPDCTFSPHSPISSNKKVFRRLTHLLKDPVPT 60
DB 1 MTVLAPAMSP--TYYLILLLLSSLSGTSQDPSFQHSPISSDPAVKIRLSYLLQDYPVT 59
QY 61 VAVNLODEKHKALMSLFLAQRWTEQLKTIVAGSKMOTLLEDVNTLHFTVCTFQPLPEC 120
DB 60 VASNLQDELCGLMRLVLAQRWMERLKTIVAGSKMGLLERVNTEHFTVTCARQPPESC 119
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVCOPDSSSTLLPPRSPALAEAT 180
DB 120 LRFVQTNISRLQFTSQDLVALKFWITR--QNFSCRLELCQCPDSSSTLLPPWSPRPLEAT 177
QY 181 ELPEPRRQQLLLLLPLTVLLAAAGLWQARARR---GELHPGVLP 228
DB 178 APTAQP--LILLLLPVGLLLAAAGLHWQRTRRTPRGEQVPPVPS 227
```

```
RESULT 9
US-09-160-841-6
; Sequence 6, Application US/09160841
; Patent No. 6190655
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match          62.8%; Score 768.5; DB 4; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MVLVAPWSPNSSLTLLLLSPCLRGTPDCYFHSPISSNFKVKFRELTDHLKDYPV 60
D 1 MVLVAPWSP--TLYLLLLSSGLSGFDSCFQHSPISSDFAVKIRELSDYLDQYPV 59
QY 61 VAVNLDEKHKRAWLSLFAQRWIEOLTVAGSKMOTLEEDVNEHFVTCAPFPPSC 120
D 60 VASNLDEELCGGLMRLVLAQRWIERLKTVAQSKMGLLENVNEHFVTCAPFPPSC 119
QY 121 LRFVQTNISHLKDTCTQLLALPCIGRACONFSRCLLEVOCOPDSSLPPRSPALEAT 180
D 120 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCLELQCOOPDSSLPPRSPALEAT 177
QY 181 ELDEPPRRQLLLLLPLTYLVLLAAAGLRRORARR---GELHGVPLP 228
D 178 APTAPQPP--LTLLLPLVGLLLAAWCLHWQRTKRRTPRGQVPPVSP 227

RESULT 10
: Sequence 1, Application US/09109100C
: Patent No. 6291661
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260, 0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Homo sapiens
```

```
US-09-109-100-1

Query Match          62.8%; Score 768.5; DB 4; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MVLVAPWSPNSSLTLLLLSPCLRGTPDCYFHSPISSNFKVKFRELTDHLKDYPV 60
D 1 MVLVAPWSP--TLYLLLLSSGLSGFDSCFQHSPISSDFAVKIRELSDYLDQYPV 59
QY 61 VAVNLDEKHKRAWLSLFAQRWIEOLTVAGSKMOTLEEDVNEHFVTCAPFPPSC 120
D 60 VASNLDEELCGGLMRLVLAQRWIERLKTVAQSKMGLLENVNEHFVTCAPFPPSC 119
QY 121 LRFVQTNISHLKDTCTQLLALPCIGRACONFSRCLLEVOCOPDSSLPPRSPALEAT 180
D 120 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCLELQCOOPDSSLPPRSPALEAT 177
QY 181 ELDEPPRRQLLLLLPLTYLVLLAAAGLRRORARR---GELHGVPLP 228
D 178 APTAPQPP--LTLLLPLVGLLLAAWCLHWQRTKRRTPRGQVPPVSP 227

RESULT 11
PCT-US94-05365-6
: Sequence 6, Application PC/TUS9405365
: GENERAL INFORMATION:
: APPLICANT: Lyman, Stewart D.
: APPLICANT: Beckmann, M. Patricia
: TITLE OF INVENTION: Ligands for FLT3/Flk-2 Receptors
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05365
: FILING DATE: May 24, 1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: -to be assigned-
: FILING DATE: May 11, 1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/209,502
: FILING DATE: March 7, 1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/162,407
: FILING DATE: December 3, 1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/111,758
: FILING DATE: August 25, 1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/106,463
: FILING DATE: August 12, 1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/068,394
: FILING DATE: May 24, 1993
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
```

```

? NAME: Malaski, Stephen L.
? REGISTRATION NUMBER: 32,655
? REFERENCE/DOCKET NUMBER: 2813-B-
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEEX: 756822
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 235 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? CSTR-US94-05365-6

```

Query Match	62.8%;	Score 768.5;	DB 5;	Length 235;
Best Local Similarity	70.3%;	Pred. No. 8e-72;		
Matches 163;	Conservative 17;	Mismatches 43;	Indels 9;	Gaps 4

[illegible]

```

RESULT 12
US-09-109-100-19
; Sequence 19, Application US/09109100C
; Patent NO. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03360.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Murine
; US-09-109-100-19

```

Query Match	59.28;	Score 724.5;	DB 4;	Length 137;
Best Local Similarity	99.38;	Pred. No. 1.4e-67;		
Matches 136; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

Qy	28	TPCQCFHSHPISNNKVFRELTHLLKDPVAVANLQD - KRHCALMSLFLAQWIEQ	86
Db	1	TPCQCFHSHPISNNKVFRELTHLLKDPVAVANLQDDEKHCALMSLFLAQWIEQ	60
Qy	87	LKTAVAGSKQQTLLBEVNTLHIFVTSCTFQPLRPLCFRFOVNTNLSHLKDTQTQLALRPI	146
Db	61	LKTAVAGSKQQTLLBEVNTLHIFVTSCTFQPLRPLCFRFOVNTNLSHLKDTQTQLALRPI	120
Qy	147	GRACONFSRCLEVCQCP	163
Db	121	GRACONFSRCLEVCQCP	137

```

RESULT 13
US-09-109-100-10
: Sequence 10, Application US/09109100C
: Patent No. 6291661
:
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGraw, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03360, 0028
: CURRENT APPLICATION NUMBER: 09/09,109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO. 10
:
: LENGTH: 212
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
: US-09-109-100-10

```

Query Match	56.68;	Score 692;	DB 4;	Length 212;
Best Local Similarity	69.98;	Pred. No. 5.7e-64;		
Matches 144;	Conservative 15;	Mismatches 39;	Indels 8;	Gaps 3

[illegible]

```

RESULT 14
US-09-109-100-15
: Sequence 15, Application US/09109100C
: Patent No. 6291661
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGraw, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03360.0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 15
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-109-100-15

```

Query Match	56.28;	Score 687;	DB 4;	Length 209;
Best Local Similarity	69.88;	Pred. No. 1.9e-63;		
Matches 143; Conservative	16;	Mismatches 38;	Indels 8;	Gaps 3

Qy	28	TPPCYSHSPISNNKVFRELTGHLIKDVPYAVANLDEKHKALISFLAORWTEOL	87
		1 TPCPSHSPISNNKVFRELTGHLIKDVPYAVANLDEKHKALISFLAORWTEOL	87
Db	1	TQPCSHSPISNNKVFRELTGHLIKDVPYAVANLDEKHKALISFLAORWTEOL	60
		1 TQPCSHSPISNNKVFRELTGHLIKDVPYAVANLDEKHKALISFLAORWTEOL	60
Qy	88	KIVAGSKMOTLLEDNEILHFVTSCTFOPLECLRFVQTNISHLKDKTOLLAKPCIG	147
		1 KIVAGSKMOTLLEDNEILHFVTSCTFOPLECLRFVQTNISHLKDKTOLLAKPCIG	147
Db	61	KIVAGSKMOTLLEDNEILHFVTSCTFOPLECLRFVQTNISHLKDKTOLLAKPCIG	120
		1 KIVAGSKMOTLLEDNEILHFVTSCTFOPLECLRFVQTNISHLKDKTOLLAKPCIG	120

```
; SOFTWARE: PatentIn Ver. 2.1
```

```

; SEQ ID NO 9
; LENGTH: 209
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-109-100-9

```

Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.3%;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3;

QY	28	TBPCEYSHSPISNNKVFRELITDHLTKDVPYAVANLQDEKHCALMSLFLAORWTEOL	87
Db	1	TQDCSHSPISSDPAVAKIRELSYDYLLODPYVAVASNLQDEELCGIWRVLYAORWMERL	60
QY	88	KTVAGSKMOTLLEEDVETIEIHVETISCTPQPLPECLRVSQVINSIHLKDKCTOGLAKPCIG	147
Db	61	KTVTGSKMQGLLEBRVNTIEHFVTKCAQPPSCGLFRVQINSIRLQETISEQVAMKFWIT	120
QY	148	KACQNSRCLTEVQOQOPOSTTLPRPSIALTEALEELPBRQRLULLLLLEPLTVILAAA	207
Db	121	R-QNSRCLTEQOQOPOSTTLPPWMSRPLPENTAPPAQPP--LULULLPLVGLDILAAA	176
QY	208	WGLRWQRARR---GELHCPVPLP	228
Db	177	WGLHWQRARRPDPGEQVPPVPSF	201

RESULT 19
US-09-109-100-12

```

1  GENERAL INFORMATION:
2  APPLICANT: Graddis, Thomas J.
3  APPLICANT: McGraw, Jeffrey T.
4  TITLE OF INVENTION: FLU-11 MUTANTS AND METHODS OF USE
5  FILE REFERENCE: 03260 0028
6  CURRENT APPLICATION NUMBER: US/09/109,100C
7  CURRENT FILING DATE: 1996-07-02
8  NUMBER OF SEQ ID NOS: 20
9  SOFTWARE: PatentIn Ver. 2.1

```

ORGANISM: Homo sapiens
US-09-109-100-12

Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.3%;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3;

[illegible]

RESULT 20
US-09-109-100-17
; Sequence 17, Application US/09109100C
; Patent No. 6291661

```

: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FIT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 17
: LENGTH: 209
: TYPE: PRT
: ORGANSIM: Homo sapiens
US-09-109-100-17

```

Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.3%;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 16;	Mismatches 39;	Indels 8;	Gaps 3,

QY	28	TPRCYSHPISINNKVFEFRETTHLKDKVPYVAVNLODEKNCALMSFLAGMSEIOL	87
Db	1	TOCCSQHPSISDPAVAKIRELSIDYLDDIPVYVANSLODEELCGMRVLAORHMERL	60
QY	88	KTVAGSKMOTLLEDVNTIEHVTSCFOPRLPECLRFVQVNIISHLKDTCTOLLAKPCIG	147
Db	61	KTVAGSKMGGLIERVNTIEHVTIEHKAFOPPPCSIRFVQVNIISRLLOETSEQVLAIPIT	120
QY	148	KACQANSKCLEVQCCPDBSSTLLPRPSFLAEATLEPRPRKOLLNLSLLEPLTVLAAA	207
Db	121	R--RNSFSKCLELQCCPDBSSTLPPWSPSPLEAATAPAPQP--LLELLLEPLVGLLAAA	176
QY	208	WGLRMQARARR---GELHPGVLP	228
Db	177	WCLHMQRTRRRKTPRPGEOVPPVPS	201

RESULT 21
US-09-109-100-11

Sequence ID, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Gradidis, Thomas J.
TITLE OF INVENTION: FLT3-L
APPLICANT: McGraw, Jeffrey T.
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02

```

; SEQ ID NO 11
; LENGTH: 209
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-109-100-11

```

Query Match	55.68;	Score 680;	DB 4;	Length 209;
Best Local Similarity	69.38;	Pred. No. 9.8e-63;		
Matches 142;	Conservative 16;	Mismatches 39;	Indels 8;	Gaps 3,

QY	28	TRPCYSBSPISNNKYKFRRLTDHKKQYRVANVANODEHKALMSLFLAARMTBOL	87
		1 TQDSQSPISPDPAKIRELSDTLDPVAVASNDDBELCGGLMRVLAQGMNRL	60
Db			
QY	88	KYVAGSKMOTLEDVNETIHHVVSCTQPLRECFRFGVQINISHLKDKPTOLLAKEFG	147
	61	KYVAGSKMOTLEDVNETIHHVVSCTQPLRECFRFGVQINISHLKDKPTOLLAKEFG	120
Db			
QY	148	KACQNFSELEVQCPDSSSTLPRSPALAEATLEPPRRQDLELLELPLTVLLAA	207
	121	R-QNFSRCLTEQCPDSSSTLPRPWSGRPLEAFAAPAPAP--LELLELLELVGILLAA	176
Db			

QY	208	WGLRWQRRARR	----	GELHPGVPLP	228
Db	177	WCLHWQTRRRTP	PRPGEQVPPVPS	201	

```

RESULT 22
US-09-109-100-13
: Sequence 13, Application US/09109100C
: Patient No. 6291661
:
: GENERAL INFORMATION:
: APPLICANT: GRADDIS, Thomas J.
: APPLICANT: McGraw, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03360.0028
: CURRENT APPLICATION NUMBER: US/09/109.100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 13
:
: LENGTH: 209
:
: TYPE: PRN
: ORGANISM: Homo sapiens
: US-09-109-100-13

```

Query Match	55.58;	Score 679;	DB 4;	Length 209;
Best Local Similarity	69.38;	Pred. No. 1.2e-62;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3

QY 28 TPQCYSHSPISNFKVFFRELTBLIKDVPVAVNLODEKCKLMSLFLQAWIOL 87
 Db 1 TQDCSQHSPISSDPAVKIKRELSDTLPDYPVAVSNLQDEELCGSLMRVLQAQMMERL 60
 QY 88 KTVAGSKMOTLEDVNTLEIHVTSCTOPRLPECLRFVQNISSHLLKDTCTOLALPKCIG 147
 Db 61 KTVAGSKMGGLLEARNVTEHFTVKCARQPPRSCSLRFQNISSHLQETSQGLVAKPMIT 120
 QY 148 KACQNSKCLEVQCCPDSSTLLPPRSPLAEATLELPEPRPROLLLSLLEPLTVLAAA 207
 Db 121 R-QNFSRCLTEIQCPDSDSTLLPPMSPPRLAEATPAQPR-LTLLLLLLPVGILLAAA 176
 QY 208 MGLRMQRRRR-----GELHPGRLP 228
 Db 177 WCLHMQRTRRRKTRPREQGVPPVPS 201

```

RESULT 23
US-09-109-100-8
: Sequence 8: Application US/09109100C
: Patent No. 6291661
:
: GENERAL INFORMATION:
: APPLICANT: GRADDIS, Thomas J.
: APPLICANT: McGraw, Jeffrey T.
: TITLE OF INVENTION: FL73-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260, 0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 8
:
: LENGTH: 209
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-09-109-100-8

```

Query Match	55.48;	Score 678;	DB 4;	length 209;
Best Local Similarity	69.38;	Pred. No. 1.6e-62;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3

QY 28 TDPCCFHSNPSSSNFKKFFELTDHLMDVPTVAANVLQDEKICAKLNSPLFLAQMTEQL 87
↑
DQ 1 TDQCQSQSPSSPSDFAVKIHRLSDYLADDPVTVAANVLQDELCGSLMRVLVLAQRMERL 60
↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑

[illegible]

```

1 RESULT 24
2 PCT-US94-05150-17
3 : Sequence 17, Application PCT/US9405150
4 : GENERAL INFORMATION:
5 : APPLICANT:
6 : APPLICANT:
7 : TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists
8 : NUMBER OF SEQUENCES: 37
9 : COMPUTER READABLE FORM:
10 : MEDIUM TYPE: Floppy disk
11 : COMPUTER: Apple Macintosh
12 : OPERATING SYSTEM: Macintosh 6.0.5
13 : SOFTWARE: Microsoft Word 5.1a
14 : CURRENT APPLICATION DATA:
15 : APPLICATION NUMBER: PCT/US94/05150
16 : FILING DATE:
17 : PRIOR APPLICATION DATA:
18 : APPLICATION NUMBER: US 08/162,413
19 : FILING DATE: 03-DEC-1993
20 : PRIOR APPLICATION DATA:
21 : APPLICATION NUMBER: US 08/155,111
22 : FILING DATE: 19-NOV-1993
23 : PRIOR APPLICATION DATA:
24 : APPLICATION NUMBER: US 08/112,391
25 : FILING DATE: 24-AUG-1993
26 : PRIOR APPLICATION DATA:
27 : APPLICATION NUMBER: US 08/106,340
28 : FILING DATE: 13-AUG-1993
29 : PRIOR APPLICATION DATA:
30 : APPLICATION NUMBER: US 08/092,549
31 : FILING DATE: 16-JUL-1993
32 : PRIOR APPLICATION DATA:
33 : APPLICATION NUMBER: US 08/089,263
34 : FILING DATE: 07-JUL-1993
35 : PRIOR APPLICATION DATA:
36 : APPLICATION NUMBER: US 08/065,231
37 : FILING DATE: 19-MAY-1993
38 : INFORMATION FOR SEQ. ID NO. 17:
39 : SEQUENCE CHARACTERISTICS:
40 : LENGTH: 42 amino acids
41 : TYPE: amino acid
42 : TOPOLOGY: linear
43 : MOLECULE TYPE: peptide
44 : PCT-US94-05150-17

```

Query Match	17.7%	Score 216;	DB 5;	Length 42;
Best Local Similarity	97.6%	Pred. No. 1.2e-15;		
Matches 41; Conservative		0; Mismatches 1;	Indels 0;	Gaps 0;

QY 28 TPDCCYFSHPSSISNFKYKPRELTDHLTKDYPVTVAVNLODEK 659
|||||
Db 1 TPDCCYFSHPSSISNFKYKPRELTVHLLKDYKPVTVAVNLODEK 422

RESULT 25
PCT-US94-05150-12
; Sequence 12, Application PC/TUS9405150
; GENERAL INFORMATION:

APPLICANT:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05150
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,549
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-05150-12

Query Match 11.0%; Score 135; DB 5; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.6e-07;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 28 TPDCYFSHSPISSNFKYKRRRLDHLK 55
DB 1 TPDAFSSHSPISSNFKVKKRELTVHLK 28

Search completed: August 6, 2002, 09:39:38
Job time: 289 sec

